

<u>S + Nam</u>	<u>Qu ry</u>		<u>Hit Count</u>	<u>S + Nam</u>
side by side				result set
	<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR</i>			
<u>L6</u>	fibrinogen adj2 binding and coagulase adj2 negative		3	<u>L6</u>
	<i>DB=USPT,PGPB,JPAB,EPAB,DWPI,TDBD; PLUR=YES; OP=OR</i>			
<u>L5</u>	fibrinogen adj2 binding and epidermidis		7	<u>L5</u>
	<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR</i>			
<u>L4</u>	(fbe or fig) adj5 gene\$ and staphylococc\$		0	<u>L4</u>
<u>L3</u>	(fbe or fig) adj5 gene\$ ans staphylococc\$		42895	<u>L3</u>
<u>L2</u>	(fbe or fig) adj5 gene\$		10	<u>L2</u>
<u>L1</u>	(fbe or fig) and epidermidis		0	<u>L1</u>

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Search Results -

Terms	Documents
fibrinogen adj2 binding and coagulase adj2 negative	3

Database: IBM Technical Disclosure Bulletins

US Patents Full-Text Database
US Pre-Grant Publication Full-Text Database
JPO Abstracts Database
EPO Abstracts Database
Derwent World Patents Index

Search:

L6

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Search History

DATE: Tuesday, July 30, 2002 [Printable Copy](#) [Create Case](#)

WEST

L3: Entry 20 of 25

File: EPAB

Oct 10, 1991

PUB-NO: DE003583987A1

DOCUMENT-IDENTIFIER: DE 3583987 A1

TITLE: TITLE DATA NOT AVAILABLE

PUBN-DATE: October 10, 1991

APPL-NO: DE03583987

APPL-DATE: October 31, 1985

PRIORITY-DATA: DE03583987A (October 31, 1985)

INT-CL (IPC): A61K 37/02; C07K 7/10; C12P 21/02

ABSTRACT:

A new antibiotic, designated epidermin (I), has the prim. structure: *Staphylococcus epidermidis* DSM 3095, which is resistant to (I), is new. (I) is made by aerobic cultivation of DSM 3095 at 34-37 deg.C on a complex nutrient soln. contg. 2-4% N source (e.g meat extract), 1-3% sugar or sugar alcohol; 0.25-1% alkaline earth carbonate and/or 0.25-0.5% alkaline earth hydroxide. The cells and inorganic salts are removed, then (I) isolated by (a) extracting with butanol at pH 8, evaporating the extract, dissolving the residue in MeOH and pptn. of lipids with ether or (b) adsorbing onto acrylic ester or polystyrene polymers, eluting with 99:1 MeOH-concn. H₂SO₄, neutralising with NH₃ and evaporating in vacuo. The isolate is then chromatographed on 'Sephadex LH-20' (RTM) to remove low mol.wt. peptides amino acid and salts, and subjected to liq-liq partitioning first in 3:1:3 n-butanol/ethyl acetate/0.1N acetic acid ((I) remaining at the starting position) and then in the neutral system 1:1 2-butanol/0.05N NH₄ acetate. Purified (I) is recovered as a colourless powder by freeze-drying.

elution with methanol/diluted hydrochloric acid, (c) the eluate is adjusted to a pH of 5.3 to 5.8, (d) the eluate is placed on a weak cation exchanger, (e) non-bound substances are subsequently washed out with a buffer solution at pH 7, (f) the active component is eluted out of the cation exchanger with a solution consisting of buffer substance, sodium chloride and methanol at pH 6.0 to 8.0 and for purification washed with water in order to remove salts and the epidermin is released from the resin with a methanol/acetic acid mixture and the solution is evaporated or freeze-dried, whilst the epidermin thus obtained may subsequently also be subjected to high performance liquid chromatography for extra purification.

CHOSEN-DRAWING: Dwg.0/10 Dwg.0/10

TITLE-TERMS: ISOLATE STAPHYLOCOCCUS CULTURE ADSORB POLYSTYRENE BASED COPOLYMER ELUTION CHROMATOGRAPHY CATION EXCHANGE USEFUL ANTIBIOTIC TREAT SKIN INFECT

DERWENT-CLASS: A96 B04 D16

CPI-CODES: A04-B10; A04-C04; A12-M03; A12-V; A12-W11L; B02-E; B11-B; B11-C08D2; B12-A07; D05-C02;

CHEMICAL-CODES:

Chemical Indexing M1 *01*

Fragmentation Code

H1	H100	H101	H181	H182	H4	H401	H481	H8	J0
J011	J012	J1	J171	J172	K0	L2	L250	M280	M311
M312	M313	M314	M315	M321	M331	M332	M333	M340	M342
M343	M349	M381	M391	M421	M510	M520	M530	M540	M620
M720	M903	N131	N161	Q233	V050	V901	V913	V923	

Ring Index

63917

Registry Numbers

1327U 0502U

POLYMER-MULTIPUNCH-CODES-AND-KEY-SERIALS:

Key Serials: 0231 0306 3162 0418 1123 2020 2569 3264 3272 2769

Multipunch Codes: 014 034 04- 055 056 074 075 077 128 231 27& 473 53& 532 533
54& 623 624 642 645 720

SECONDARY-ACC-NO:

CPI Secondary Accession Numbers: C1990-006930

WEST

L3: Entry 24 of 25

File: DWPI

Jun 10, 1997

DERWENT-ACC-NO: 1990-016158

DERWENT-WEEK: 199944

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TITLE: Isolating epidermin from staphylococcus epidermidis culture - by adsorption on styrene! based copolymer, elution and chromatography on cation exchanger, useful as antibiotic for treating skin infections

INVENTOR: FIEDLER, H; HOERNER, T; JUNG, G; KELLNER, R; WERNER, R; ZAEHNER, H; FIEDLER, H P; HORNER, T; KELLNER, J R; WERNER, R G; ZAHNER, H

PATENT-ASSIGNEE:

ASSIGNEE	CODE
THOMAE GMBH KARL	THOM

PRIORITY-DATA: 1988US-0219698 (July 15, 1988)**PATENT-FAMILY:**

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
KR 9709289 B1	June 10, 1997		000	C07K001/14
EP 350810 A	January 17, 1990	G	018	
AU 8938103 A	January 18, 1990		000	
PT 91171 A	February 8, 1990		000	
DK 8903506 A	January 16, 1990		000	
JP 02084194 A	March 26, 1990		000	
ZA 8905362 A	March 27, 1991		000	
EP 350810 B1	September 29, 1993	G	021	C07K001/14
DE 58905744 G	November 4, 1993		000	C07K001/14
ES 2059645 T3	November 16, 1994		000	C07K001/14
IE 62402 B	January 25, 1995		000	C07K001/14
CA 1336896 C	September 5, 1995		000	C12P021/02
JP 2777205 B2	July 16, 1998		012	C12P021/02

DESIGNATED-STATES: AT BE CH DE ES FR GB GR IT LI LU NL SE AT BE CH DE ES FR GB GR IT LI LU NL SE

CITED-DOCUMENTS: 1.Jnl.Ref; A3...9139 ; EP 181578 ; EP 27710 ; No-SR.Pub

APPLICATION-DATA:

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
KR 9709289B1	July 15, 1989	1989KR-0010095	
EP 350810A	July 7, 1989	1989EP-0112446	
JP02084194A	July 14, 1989	1989JP-0182372	
ZA 8905362A	July 14, 1989	1989ZA-0005362	
EP 350810B1	July 7, 1989	1989EP-0112446	
DE58905744G	July 7, 1989	1989DE-0505744	
DE58905744G	July 7, 1989	1989EP-0112446	
DE58905744G		EP 350810	Based on
ES 2059645T3	July 7, 1989	1989EP-0112446	
ES 2059645T3		EP 350810	Based on
IE 62402B	July 14, 1989	1989IE-0002283	
CA 1336896C	July 14, 1989	1989CA-0605673	
JP 2777205B2	July 14, 1989	1989JP-0182372	
JP 2777205B2		JP 2084194	Previous Publ.

INT-CL (IPC): A61K 0/00; C07G 11/00; C07K 1/14; C07K 3/12; C07K 7/10; C07K 15/04; C07K 17/10;
C12N 11/08; C12P 1/04; C12P 21/02; C12R 1/45; C12P 21/02; C12R 1/45; C12P 21/02; C12R 1/45

ABSTRACTED-PUB-NO: EP 350810A

BASIC-ABSTRACT:

the polypeptide antibiotic epidermin (I) is isolated and purified from a culture of a Staphylococcus epidermidis strain by (a) applying the culture broth or filtrate to a styrene-divinyl copolymer (A), (2) eluting active ingredients with MeOH-dil HCl, (3) adjusting eluate to pH 5.3-5.8; (4) applying to a weak cation exchanger (B) (5) washing-out non-bound cpds. with pH7 buffer, (6) eluting (I) with pH 6-8 buffer contg. and MeOH, (7) readsorbing (I) onto (A) washing the resin with water (desalting) and eluting with MeOH-MeCOOH mitd., (8) evaporating or freeze-drying the eluate, and opt. (9) further pruifying by h.p.l.c.

The S. epidermidis strains used are pref. DSM 3095 or NC18 11536.

USE/ADVANTAGE - (I) is known for treatment of skin infections such as eczema, impetigo, cellulitis and acne. This method is simple and produces significantly higher yields of (I) then known processes.
ABSTRACTED-PUB-NO:

EP 350810B

EQUIVALENT-ABSTRACTS:

Process for isolating epidermin from a culture broth or a culture filtrate of a strain of Staphylococcus epidermidis and for purifying this substrate, characterised in that (a) the culture filtrate or culture broth is added to a styrene-divinyl copolymer, (b) the active component is released from the resin by

A; Reference number: S41539; MUID:94224142

A; Accession: S41539

A; Status: preliminary

A; Molecule type: DNA

A; Cross-references: EMLU:Z18852; NID:9397525; PID:CAA79304.1; PID:g397526

Query Match 15.9%; Score 490; DB 2; Length 953;

Best Local Similarity 28.6%; Pred. No. 7.7e-14; Gaps 22; Matches 162; Conservative 83; Mismatches 236; Indels 94; Gaps 22;

Qy 42 GIEKNSEDRTESTTNDENATEFLQKTPQDNTLHTEEEVKESSSESSNSSIDTAQQPSHTINREESVOTSDNVEDSHVSDFANS 101

Db 45 GHEAKKAHEHTGELNQSKNETT---APSENK--TTEKV--D6EROKDNTQATADQPKV 95

Qy 102 TTINRBESVQTSDNVEDSHVSDFANSKIKESNTESGKENTIEPNKVKREDSTSQPSGY 151

Db 97 T-----MSDASATVKERSSMOS-----PONATASQSTQTSNV 129

Qy 162 TNIDEK---ISNQDELLNLPINEYEN-KARPLSLSTAQPSIKRTVNOLAA-EQCSNVNH 216

Db 130 TTNDKRSITVSNETDKSNU---TQAKNVSITPKTTIKQRALNFMAVNTVAAPDQGTNVND 187

Qy 217 LKVTPDII-----TEGVDDSGVKGIAHDAENLIVDVTFEVNDDKVKGSDTM 263

Db 188 KWHFTNIDIAKDGHKHNKTGCTNIEFWATSSDVLK-----LKANYTIDDSVKGDT 239

Qy 264 VD1DKWNPSPDLDSTIPKIKDNSEIITGTYPDKNKRQITYPTDYDVKYENIKAHK 323

Db 240 FRYGQYFRPGSVRLPSQTONLYNAQGNILAKGYDLSKNTNTYTFNVDQYTIVNGSF 299

Qy 324 LTSIDKSKVPPNNTKLDEVKTLASSVNUITVEQRPFENFTANLQSMETNDTKH 383

Db 300 QVAFAKRENATTDKTAYKMEVTLGNDTYSKOIVN--GNOQKGOOLISSTNYINNEDS 356

Qy 384 VEQTITIN-PURYSAKETNVNISGNGDEGSTIIDSTTICKVYKGDQNQLPDSRIYD 441

Db 357 RMMTVVYQNPKKTYTRETFVNLT----GYKFNDAKNPKIYETDQNOFUDS-FTPDT 410

Qy 442 SEYEDVYND-DYAOLGNNNDVNINFGN---IDSPYIYKIVSKYPPNKDDYTTQOOTVM 496

Db 411 SKLKDVTGQFDWYISNDNKTATVDLNGQSSSDQKQYIQOYAPDSNSTDNGKIDYLET 470

Qy 497 OTTINBYTGERFTASYNTIAFSTSSQGQGDLPPEKTTIGYVWEDVQDGONTND 556

Db 471 ONGKSSWN---SYNSVNGNSTANGD----OKKYNLGCVWEDTNKGKODA--N 516

Qy 557 ERPLSNLVLTYPDGTS-KSVRTEBDGK*QFDGV 590

Db 517 EKGIGKVYVILKDSNGKELDRTTDENGKVQFTGL 551

Qy 92 NP-----AQQETQSSSPNATNEETPTVGEATTTQNANTPATOS-SWYNAEELVN 143

Db 128 KIKBSNTESGKEEINTIEOPNKVKEDSTSOPSGYNTIDEKISNQDELLN-LPINEVNAA-196

Db 144 --QTSNETTFNDNTV-----SSVNPQNSTNAENSTQDSTEAPSNC--NES 189

Qy 187 RPLSTTSQAPSISKRTVN-----QLAACEGGSNTNHLKVTDO--S1BEGDSEGV 235

Db 190 APOSDASHKDVNVQAVNSAPRMRAFSLAVADAPAGTDITNQLNQJNTVYGI-DSGT 248

Qy 236 IKAHDARENIIYDVFEVDDKVKSGDTMTWDIDKNTVPSLTSFTIKRDKNSGEIATG 295

Db 249 VPRHAGYVKNIGFSVPNSAVKGDTKTFITVPRKELNLUQVTPAKVPRIMAGD-QVLANG 307

Qy 296 TYDNRNKQITYTFDVKYENIKAHLKLTSYIDSKVPPNNKL-DVEYKTALESS--VN 352

Db 308 VIDS-DGNVYIYTFDYNKDDYKATLTPAYD---PENVKTGNTVATGIGSTAN 362

Qy 353 KTRTVEYORPBNRNFANLQSMETNDTKHVTQSOIYINPL--RYSAKETNNTNISGDE 410

Db 363 KTBLVYDYEKGKFYKFLNSIGKTIDQDQTKNTYRQTYVNPSPGDNVIAPLVTLGNLKPNTD 422

Qy 411 GSTIIDDSTTICKVYKGDQNQLPDSRIYDSEYDVNDDYQOLGNNDVNINFQ---- 466

Db 423 NALIDQONNTISIKVYKVDNAHDLSFYV-NPENFEDVTSVNITFPNPQKYEVNTPD 481

Qy 467 NIDSPYIYKIVSKYDPN-KDVTIQTQYTMQTTINETGE--FRTAQSYNTIAFSSSG 523

Db 482 QITTRYIVWVNGHIDPNSKG----DALSPLYGNUNNIWRSMSWDNEVAFNINGSG 534

Qy 524 OGQG-DLP--PEKTYKIGD--WMBDVID-GIONTND 556

Db 535 SGDGDIDKPVVPEQDPEGEPIPEDSDSDPGSDSGSDS 573

RESULT 7

S41539 fibrinogen-binding protein - *Staphylococcus aureus*N:Alternate names: clumping factor
C:Species: *Staphylococcus aureus*
C:Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text_change 15-Oct-1999
C:Accession: S41539; S35630
R:McDevitt, D.; Francois, P.; Vaudaux, P.; Foster, T.J.Mol. Microbiol. 11, 237-248, 1994
Title: Molecular characterization of the clumping factor (fibrinogen receptor) of *Stap-*

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OM protein - protein search, using sw model.

Run on: July 30, 2002, 10:28:50 ; Search time 85.16 seconds
{without alignments}
773.447 Million cell updates/sec

Title: US-09-147-405-11.
Perfect score: 3087
Sequence: HHHHHHPSDEERNDVNN.....SKSYRTDEDGKYQFDGVQVD 593

Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032803:*

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2: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*

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11: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*

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15: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*

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18: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*

21: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

22: /SIDS1/gcdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	3015	97.7	1092	19 AAU41602
2	2812.5	91.1	991	21 AAY83171
3	2012.5	91.1	991	21 AAU70120
4	1146.5	37.1	1166	20 AAY08543
5	857	27.8	22 AAG8203	
6	576	18.7	1315	20 AAY08624
7	576	18.7	1349	22 AAU34402
8	576	18.7	1349	22 AAU37544
9	506	16.4	1802	21 AAY83170
10	506	16.4	1802	21 AAY70119
11	504	16.3	1155	22 AAG82343

ALIGNMENTS

RESULT ID	AAW1602	AAW1602 standard; Protein; 1092 AA.
ID	AAW1602	
XX		
AC	AAW1602;	
XX		
DT	22-JUN-1998 (first entry)	
DE	Staphylococcus epidermidis fibrinogen binding protein FIG.	
XX		
KW	Fibrinogen binding protein; FIG; aggregation; infection;	
KW	coagulase-negative Staphylococcus; therapy; diagnosis;	
KW	immunisation; immunogen; vaccine.	
XX		
OS	Staphylococcus epidermidis strain HB.	
XX		
FR	key Location/Qualifiers	
FT	peptide 1..51	
FT	/label= Sig-peptide	
FT	Protein 52..1092	
FT	/label= Mat_protein	
FT	Region 52..824	
FT	/note= "non-repetitive region, harbours fibrinogen binding activity"	
FT	Region 825..1040	
FT	/note= "Asp-Ser dipeptide repeat region"	
FT	Region 1053..1057	
FT	/note= "cell wall anchoring motif"	
XX		
PN	W09748727-A1.	
PD	24-DEC-1997.	
PP	18-JUN-1997;	97WO-SE01091.

PR 20-JUN-1996; 96SE-0002496. Db 555 ttiqqtqvumqtinneytgeftrasyntiafssggggdlpeptkikgdywvedvk 61
 XX PA (FLOC/) FLOCK J. QY 548 DGIQNTNDNEKEPLISNVLUTLYPDGTSKSVRTBEDGKTOFDGVO 591
 PA (FRYK-) FRYKBERG L. DB 615 dgigntndnekeplsnvivtlypdgtsksvrtaedgkyqfdgk 658
 PA (GUSS/) GUSS B.
 PA (LIND/) LINDBERG M.
 PA (NILS/) NILSSON M.
 XX PI Flock J., Frykberg L., Guss B., Lindberg M., Nilsson M;
 XX DR WPI; 1998-063079-06.
 DR N-PSDB; RAV04279.
 XX PT fibrinogen-binding protein from coagulase-negative *Staphylococcus* -
 used for prevention, treatment and diagnosis of *Staphylococcus* -
 PT infection.
 XX Example 3; fig 6; 45PP; English.
 XX The protein comprises the fibrinogen binding protein (FIG) of
 coagulase-negative *Staphylococcus epidermidis* HB. Its amino
 acid sequence was deduced from the isolated FIG gene (see RAV04279).
 CC The closest known analogue of FIG is the clumping factor of
 S. aureus which also binds fibrinogen and promotes bacterial
 CC aggregation in serum. Recombinant FIG polypeptides can be
 expressed in host cells. They are used as immunogens, particularly
 CC in vaccines (which may be expressed *in vivo*) to protect humans and
 CC animals against coagulase-negative *Staphylococcus* infection.
 CC Antibodies raised against FIG can be used for passive immunisation.
 CC They block the adherence of bacteria) and for diagnosis.
 XX Sequence 1092 AA;
 SQ

RESULT 2
 AAY83171 ID AAV83171 standard; Protein; 991 AA.
 XX ID AAV83171
 AC AAY83171;
 XX DT 24-JUL-2000 (first entry)
 XX DE Cell wall protein SdrG.
 XX KW SdrF; SdrG; SdrH; coagulase negative; staphylococcus; septicemia;
 KW osteomylitis; endocarditis; immune response; vaccine; graft;
 KW stent; intravenous catheter; heart valve; cardiac.
 XX OS *Staphylococcus* sp.
 XX FH Key Location/Qualifiers
 FT Misc-difference 14 /note= "Position encoded by TAG stop codon"
 FT Misc-difference 33 /note= "Position encoded by TGA stop codon"
 FT Misc-difference 964 /note= "Position encoded by TAA stop codon"
 FT Misc-difference 980 /note= "Position encoded by TAG stop codon"
 FT Misc-difference 989 /note= "Position encoded by TAA stop codon"

Query Match 91.1%; Score 2812.5; DB 21; Length 991;
 Best Local Similarity 93.3%; Pred. No. 4.4e-14; FT
 Matches 545; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

OY 8 SSDEEKNDVINYNNQSNINTDDNNOLIKKEETNNYDGIERSEDETESTINDENEATELQK 67
 ||:|||||:|||||:|||||:|||||:|||:|||:|||||:|||||:|||||:
 Db ssneekndvinynnqsnintddnnolikkeetnnydgersedelestindeneateflqk 164
 XX PD 09-MAR-2000.
 XX PA 31-AUG-1999; 99WO-US19727.
 PR 31-AUG-1998; 98US-0098439.
 XX PA (INHI-) INHIBEX INC.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (DOEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
 XX PI Pattie JM, Foster TJ, Hook M;
 DR WPI; 2000-237781/20.
 DR N-PSSB; AAZ51202.

OY 68 TPQDNTLHTEEEKEKESSESSNESSNSIDTAQQSHTTINRESEWTSDNVEDSHVSDFANS 127
 |||:|||||:|||:|||||:|||||:|||||:|||:|||||:|||||:
 Db tpqdnqkveekvkepsvessnsmsdaqqphttseasqtsseensvsdfans 224
 XX PT Composition used for generating immune response or for inhibiting
 microbial colonisation in an animal comprises antibodies that bind
 PT fibronectin binding protein and, optionally,
 PT fibronectin binding protein -
 XX PS Claim 8; Fig 4; 115pp; English.

OY 128 KIKRSNTESGKENTIQPNKVKEDSTMOPSGYTNTIDEKISNODELNLPINEYENKAR 187
 |||:|||||:|||||:|||||:|||||:|||||:
 Db kilesnteskeentiedpnkvredstsqspsyknideksinqdelnlpineyenkar 284
 XX PT The patent discloses multicomponent vaccines containing selected
 CC combinations of bacterial binding proteins termed MSCRAMM (microbial
 CC surface components recognising adhesive matrix molecules) or their
 CC antibodies. A vaccine composition is provided that includes collagen
 CC binding protein or peptide, e.g., CNA, a fibrinogen binding Protein
 CC preferably Clumping factor A (CfA) or Clumping factor B (CfB),
 CC and optionally a fibronectin binding protein e.g. FnBP-A.
 CC The vaccines are useful for imparting protection against a broad
 CC spectrum of Staphylococcal strains and for inhibiting microbial
 CC colonisation, especially of Staphylococcus aureus, in an animal.
 CC The combinations can also be used to select donor blood pools for the
 CC preparation of purified blood products for passive immunisation.
 CC The present sequence is a serine-aspartate repeat region
 CC protein, SdrG from Staphylococcus epidermidis. The Sdr protein is
 CC useful in vaccine preparation in combination with specific
 CC bacterial binding proteins. These vaccines can be used to treat a broad
 CC spectrum of bacterial infections, including those arising from both
 CC coagulase-positive and coagulase-negative bacteria.
 XX Sequence 991 AA;

RESULT 3
 AAY70120
 D standard; Protein: 991 AA.
 AAY70120:
 AC
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Staph. epidermidis serine-aspartate repeat region protein SdrG.
 KW Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;
 KW microbial surface components recognising adhesive matrix molecules;
 KW collagen binding protein; Cbp; Cna; fibrinogen binding protein;
 KW Clumping factor A; CfA; Clumping factor B; CfB; Fnbp;
 KW fibronectin binding protein; Staphylococcus infection;
 KW serine-aspartate repeat region protein; Sdr protein; SdrG.
 XX
 OS Staphylococcus epidermidis.
 FH Key Location/Qualifiers
 FT Misc-difference 14
 FT /note- "Encoded by in-frame stop codon TAG"
 FT Misc-difference 33
 FT /note- "Encoded by in-frame stop codon TGA"
 FT Misc-difference 964
 FT /note- "Encoded by in-frame stop codon TAA"
 FT Misc-difference 980
 FT /note- "Encoded by in-frame stop codon TAG"
 FT

Query Match 91.1%; Score 2812.5; DB 21; Length 991;
 Best Local Similarity 93.3%; Pred. No. 4.4e-14; FT
 Matches 545; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

OY 8 SSDEEKNDVINYNNQSNINTDDNNOLIKKEETNNYDGIERSEDETESTINDENEATELQK 67
 ||:|||||:|||||:|||||:|||||:|||:|||:|||||:|||||:
 Db ssneekndvinynnqsnintddnnolikkeetnnydgersedelestindeneateflqk 164
 XX PD 09-MAR-2000.
 XX PA 31-AUG-1999; 99WO-US19727.
 PR 31-AUG-1998; 98US-0098439.
 XX PA (INHI-) INHIBEX INC.
 PA (TEXA) UNIV TEXAS A & M SYSTEM.
 PA (DOEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
 XX PI Pattie JM, Foster TJ, Hook M;
 DR WPI; 2000-237781/20.
 DR N-PSSB; AAZ51202.

OY 128 KIKRSNTESGKENTIQPNKVKEDSTMOPSGYTNTIDEKISNODELNLPINEYENKAR 187
 |||:|||||:|||||:|||||:|||||:
 Db kilesnteskeentiedpnkvredstsqspsyknideksinqdelnlpineyenkar 284
 XX PT The patent discloses multicomponent vaccines containing selected
 CC combinations of bacterial binding proteins termed MSCRAMM (microbial
 CC surface components recognising adhesive matrix molecules) or their
 CC antibodies. A vaccine composition is provided that includes collagen
 CC binding protein or peptide, e.g., CNA, a fibrinogen binding Protein
 CC preferably Clumping factor A (CfA) or Clumping factor B (CfB),
 CC and optionally a fibronectin binding protein e.g. FnBP-A.
 CC The vaccines are useful for imparting protection against a broad
 CC spectrum of Staphylococcal strains and for inhibiting microbial
 CC colonisation, especially of Staphylococcus aureus, in an animal.
 CC The combinations can also be used to select donor blood pools for the
 CC preparation of purified blood products for passive immunisation.
 CC The present sequence is a serine-aspartate repeat region
 CC protein, SdrG from Staphylococcus epidermidis. The Sdr protein is
 CC useful in vaccine preparation in combination with specific
 CC bacterial binding proteins. These vaccines can be used to treat a broad
 CC spectrum of bacterial infections, including those arising from both
 CC coagulase-positive and coagulase-negative bacteria.
 XX Sequence 991 AA;

RESULT 3
 AAY70120
 D standard; Protein: 991 AA.
 AAY70120:
 AC
 XX
 DT 06-JUN-2000 (first entry)
 XX
 DE Staph. epidermidis serine-aspartate repeat region protein SdrG.
 KW Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM;
 KW microbial surface components recognising adhesive matrix molecules;
 KW collagen binding protein; Cbp; Cna; fibrinogen binding protein;
 KW Clumping factor A; CfA; Clumping factor B; CfB; Fnbp;
 KW fibronectin binding protein; Staphylococcus infection;
 KW serine-aspartate repeat region protein; Sdr protein; SdrG.
 XX
 OS Staphylococcus epidermidis.
 FH Key Location/Qualifiers
 FT Misc-difference 14
 FT /note- "Encoded by in-frame stop codon TAG"
 FT Misc-difference 33
 FT /note- "Encoded by in-frame stop codon TGA"
 FT Misc-difference 964
 FT /note- "Encoded by in-frame stop codon TAA"
 FT Misc-difference 980
 FT /note- "Encoded by in-frame stop codon TAG"
 FT

ID AAG82803 standard; Protein; 278 AA.
 XX
 AC AAG82803;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE S. epidermidis open reading frame protein sequence SEQ ID NO:2700.
 XX
 KW Staphylococcus epidermidis SRI strain; infection; diagnosis;
 KW vaccination; endocarditis.
 XX
 OS Staphylococcus epidermidis.
 XX
 WO200134809-A2.
 PN
 PD 17-MAY-2001.
 XX
 09-NOV-2000; 200000-US30782.
 PF
 09-NOV-1999; 99US-0164258.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 FI Kimerly RJ;
 XX
 WPI; 2001-316495/33.
 DR N-PSDB; AAH53653.
 XX
 PT Nucleic acids encoding Polypeptides from *Staphylococcus epidermidis*, useful for vaccinating against infections, e.g. endocarditis.
 XX
 PS Claim 18; Page 705; 2189pp; English.
 PR
 AAH2304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from *Staphylococcus epidermidis*.
 CC (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the
 CC *S. epidermidis* polypeptides (II) via the production of vectors containing them which are used to produce host cells which express the
 CC polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of *S. epidermidis* infections, e.g. endocarditis. AAH53971 to AAH53970 represent specifically claimed *S. epidermidis* genomic DNA poly nucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
 CC N.B. The present invention specifically claims all the poly nucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
 CC Sequence 278 AA;
 XX
 Query Match 27.8%; Score 857; DB 22; length 278;
 Best Local Similarity 93.0%; Pred. No. 4; 4e-39;
 Matches 172; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
 QY 8 SSDEEKNDVNTNINOSINTDDNNQIKKEETNYDGTEKRSERDTTESTNTDNEATFLQK 67
 Db 75 ssdeekndvnnqnsinsdnnqinkkeetndgkssedrtestnvdeneatflqk 134
 QY 68 TPDQDNTHLTEREEVKESSVSESSNSDTAQPSHTTINRESESQISDNVEDSHVSDFANS 127
 Db 135 sqpdnhtleeevkessvssnsidtaqpshttlnreessqtsdnvedshvsdfans 194
 QY 128 KIKESENTEGKENTEQPNKVKEDSTTSOPSGYTNTDEKISQNQDELNLNPINEYENKAR 187
 Db 195 kkesntesgkeentieqnkvkedttsqsgytnidekisnqdelnlpiner--kvt 252

QY 188 PLSTTT 192
 QY ||| |
 Db 253 klsvt 257

RESULT 6
 AAY08642 ID AAY08642 standard; Protein; 1315 AA.
 XX
 AC AAY08642;
 XX
 DT 09-AUG-1999 (first entry)
 XX
 DE S. aureus SdrE protein.
 XX
 KW Fibrinogen-binding protein; alpha chain; beta chain; ClfB; SdrC; SdrD;
 KW SdrE; fibrinogen; medical device; competitive inhibitor; pharmaceutical;
 KW treatment; infection; septicemia; osteomyelitis; mastitis; endocarditis;
 KW extracellular matrix; vascular graft; vascular stent; vaccine;
 KW intravenous catheter; artificial heart valve; cardiac assist device;
 KW antibacterial.
 XX
 OS Staphylococcus aureus.
 XX
 PN WO927109-A2.
 XX
 PD 03-JUN-1999.
 XX
 PR 25-NOV-1998; 98WO-US2246.
 XX
 PR 31-AUG-1998; 98US-0098427.
 PR 26-NOV-1997; 97US-0066815.
 XX
 PA (EIDH/ EIDHIN D N.
 PA (FORF-) FORFAS T/A BIORESEARCH IRELAND.
 PA (FOST-) FOSTER T J.
 PA (HOOK-) HOOK M A O.
 PA (INH1-) INHIBITEX INC.
 PA (JOSE-) JOSEFSSON E.
 PA (PATT-) PATTI J M.
 PA (PERK-) PERKINS S E.
 XX
 PI Eidkin DN, Foster TJ, Hook MA, Josefsson E, Patti JM;
 CC PT
 XX
 DR WPI; 1999-357844/30.
 PR N-PSDB; AAX277593.
 XX
 PI Eidkin DN, Foster TJ, Hook MA, Josefsson E, Patti JM;
 CC PT
 XX
 PS Claim 8; Fig 8; 143pp; English.
 XX
 CC This invention describes novel *Staphylococcus aureus* fibrinogen-binding proteins that bind both the alpha and beta fibrinogen chains. The CC proteins (and their encoding nucleic acids) are ClfB, SdrC, SdrD and SdrE. *Staphylococcus aureus* is thought to utilize fibrinogen to adhere CC to medical devices, binding proteins that bind both the alpha and beta CC fibrinogen chains (ClfB, SdrC, SdrD and SdrE) can therefore be used as CC competitive inhibitors to block this binding. Antibodies against ClfB, SdrC, SdrD and SdrE inhibit ClfB, SdrC, SdrD and SdrE mediated binding. CC The proteins of the invention can be used in a pharmaceutical composition CC for the treatment of *Staphylococcus aureus* infection, e.g. septicemia, osteomyelitis, mastitis or endocarditis or to inhibit the binding of CC *S. aureus* to the extracellular matrix. The proteins or their fragments CC may be used to coat a medical device to reduce the *S. aureus* infection of CC an indwelling medical device, especially where the medical device is CC selected from the group consisting of vascular grafts, vascular stents, CC intravenous catheters, artificial heart valves and cardiac assist CC devices. ClfB, SdrC, SdrD, SdrE, or an active fragment, subdomain or CC encoding gene, may be used as a vaccine. The DS (aspartate serine) repeat CC region or a gene encoding it may be used as an identifying probe for the identification of genes and encoding proteins from *Staphylococcus aureus*

QY	SUNKTIVYQRPN--ENRTRANLQSMFTNDTKNHT-----VEQTINYPLRSAKE	399
:	: : : : : : : : : : : : : :	
Db	nttktttanlqppdyvneeknsaft--etvhvgnkenpsyykqtlyvnppensln	439
QY	TNVNI---SGNGDEGSTIDSTIJKVKGDNQNLPPDSNRXIDYD--EYDVTNDVA	453
:	: : : : : : : : : : : : : :	
Db	aklvqayhssyppnqinkdtdikyqvpkgyl--nkgqvdtln-qyl	495
QY	Q---LGNNNDVNINFGNIDSPYKTVKLYKDPMKDPNKKDWTMTOQTMWQTINNEYGEFRTA	510
Db	qktyggnnsavifgngadsayvmvntkfqytusestplvqmatlssgn----ksv	549
QY	SYDNTIAFSTSSGQQGQGPPLPEPKTYKIDGYWEDVDKGQINTNDNEKPLSNUVLTYP	570
:	: : : : : : : : : : : :	
Db	550 stgnaqfttngsqgag---gevykqignywedtnknqygel--gekvgvntvvtv-fd	602
OY	571 DGTSKSR--TDEDGKY	585
:	: : : : : : : : : : : : : :	
PA	603 nntntkvgeavtkegsy	620
RESULT	8	
ID	AAU37544	
TD	standard; Protein; 1349 AA.	
XX		
AC	AAU37544;	
XX		
DT	14-FEB-2002. (first entry)	
DE	Staphylococcus aureus cellular proliferation protein #1714.	
XX		
KW	Antisense; prokaryotic cellular proliferation protein;	
KW	antibiotic; antibacterial; drug design.	
XX		
OS	Staphylococcus aureus.	
OS		
XX		
PN	WO200170955-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	21-MAR-2001; 2001WO-US09180.	
XX		
PR	21-MAR-2000; 2000US-191978P.	
PR	23-MAY-2000; 2000US-206448P.	
PR	26-MAY-2000; 2000US-207727P.	
PR	23-OCT-2000; 2000US-242578P.	
PR	27-NOV-2000; 2000US-253025P.	
PR	22-DEC-2000; 2000US-257931P.	
PR	16-FEB-2001; 2001US-269308P.	
XX		
PA	(ELIT-) ELITRA PHARM INC.	
XX		
PI	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Travick JD, Carr GJ;	
PI	Yamamoto RT, Xu HH;	
XX		
DR	WPI: 2001-611495/70.	
DR	N-PSDB; AAS55403.	
XX		
PT	New polynucleotides for the identification and development of	
PT	antibiotics, comprise sequences of antisense nucleic acids -	
XX		
PS	Example 3: seq ID No 13137; 51pp; English.	
XX		
CC	The invention relates to antisense inhibitors of genes essential to	
CC	prokaryotic cellular proliferation, their use in identifying the	
CC	genes, their use in the discovery of novel antibiotics, the essential	
CC	prokaryotes and the encoded proteins. The prokaryotes used are	
CC	Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella	
CC	pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The	
CC	invention is also useful for the identification of potential new targets	
CC	for antibiotic development. The antisense nucleic acids can also be used	

identify proteins used in proliferation, to express these proteins, to obtain antibodies capable of binding to the expressed proteins. Proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein.

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

wipo.int/pub/published-pct-sequences.

XX	SdF; SdR; SdR; coagulase negative; staphylococcus; septicemia; osteomyelitis; endocarditis; immune response; vaccine; graft; stent; intravenous catheter; heart valve; cardiac.
KW	staphylococcus sp.
OS	
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 12 /note= "Position encoded by TAA stop codon"
FT	Misc-difference 28 /note= "Position encoded by TAA stop codon"
FT	Misc-difference 1771 /note= "Position encoded by TGA stop codon"
FT	Misc-difference 1774 /note= "Position encoded by TGA stop codon"
FT	Misc-difference 1793 /note= "Position encoded by TAA stop codon"
FT	Misc-difference 1800 /note= "Position encoded by TAA stop codon"
FT	Misc-difference 1800 /note= "Position encoded by TGA stop codon"
FT	WO200012689-A1.
PD	09-MAR-2000.
XX	31-AUG-1999; 99WO-US19728.
PF	PR 31-AUG-1998; 99US-0098443.
PR	PR 25-JAN-1999; 99US-0117119.
XX	(QUEE-) QUEEN ELIZABETH COLLEGE DUBLIN.
PA	PA (TEXA) UNIV TEXAS A & M SYSTEM.
XX	Foster TJ, Hook M, Davis S, Hartford O, McCreary K, Ni Eldhin D;
DR	DR WPI; 2000-256637/22.
PT	PT N-PSPB; AA293533.
XX	PT Recombinant or synthetic proteins from coagulase-negative staphylococci useful for prevention, treatment and diagnosis of staphylococcal infections bind soluble and immobilized fibrinogen
XX	PS Claim 2; Figure 2; 104pp; English.
CC	CC Isolated Staphylococcus sdr cell wall proteins which bind both soluble and immobilized fibrinogen are useful for treating or preventing coagulase-negative staphylococcal infection such as septicemia, osteomyelitis or endocarditis, and for inducing immune responses in patients. The cell wall proteins are also useful for reducing coagulase-negative staphylococci infection of indwelling medical devices such as vascular grafts, vascular stents, intravenous catheters, artificial heart valves and cardiac assist devices. The cell wall associated proteins are able to inhibit staphylococcal adhesion to immobilized extracellular matrix or host cells present on the surface of implanted biomaterials.
XX	XX Sequence 1802 AA;
Query	Match 16.4%; score 505; DB 21; Length 1802; Best Local Similarity 27.4%; Pred. No. 4.9e-19; Matches 174; Conservative 101; Mismatches 276; Indels 84; Gaps 27;
Db	172 ptvnneesiactptktatqgstekekonsi-kdn-nssts-skashtdskqaqmstnk 230
Oy	55 TNVDENEA-TFLQKRP-PODWTMHLREEVKSSSVSNS-----SDTAQOPSHRT 103
Dy	231 sldtndspqsektsqandstnqsaqskqlskpqsqkvyytkfnepgtavent 290
Oy	104 IN-RESEVOVDSNVEDSHVSDFANSKIKSNTESCEKEENTIEQPNVKUEDSTTSGCT 162
Db	291 tkktpsvstddsvndk--qdvrsv---aslgdsneteaittavrdnlkaesre 344
Qy	163 NIDEKI-----SNODELLNP---TNEYENKARPLSTSQAQPSIKRVTWMLAE-- 209
Db	345 ginealaealkdfsnpsdygvatplainrsqsknsp--hksasp--immlnslaepn 399
Qy	210 QGNVNHJLKVTOO--S-TEGYDSEGVKAHAENLYDVTEFDDVKVKGOMTMVID 267
Db	400 sgknvndkvkituptlsinksnnhanniywptsneqfnlkanyellddsikegftiky 459
Qy	268 KNTVPSDUDTSFRKPKIKDNNGEATGTYDKNNKQRTFTDVDKENIKAHLKLSY 327
Db	460 qyirpggelpaktqkrsdgavnygdkttnttyftriydqgqntafat 519
Qy	328 IDKSKVPNNNTKLVEYKTAALSVNKTTIVEXORPNEANTANLOSMFNTIDTKNTVHQ 387
Db	520 pkretalkdnqnpymevtianevvkkdfivdyunkkdtt--aavanvdvnnkhnev 576
Qy	388 IYNPLRS-RAKEINVNISNGDGSTTIDSTI--INVYKVDNQNRDS-NRIVDSE 443
Db	577 vyinqnqnqnpkyaky-----fstvkngefipgevkvyevdtnawdsfpdlssn 628
Qy	444 YEDVTDNDYAQ-L-GNNNDVNINGNI--DSPVIKVISKYDPNKKDDYTIGOTVTMOTT 499
Db	629 vdrvtqfapksadgtqvdtfarasnangkyltvqavrpqgtayt-egwlttgt 666
Qy	500 INBYTGERPRTASYDNTAFSTSSGGODLPPKTYKGDDYWWEDVDDKGIONTNNDNKP 559
Db	687 tn-tndryrgktsttvtylingsstaaqgdnp--tysigaywldknknqvg--dddekg 739
Qy	560 LSNVLYTUTYPOTSK--VRDDEGXYQDFQV 591
Db	740 lagvyvtl--kdsnnrelqrvttdqsghyqfdnq 772
RESULT 10	
ID	AAY70119
XX	AAY70119 standard; Protein; 1802 AA.
AC	AAY70119;
XX	
DT	06-JUN-2000 (first entry)
XX	
DE	Staph. epidermidis serine-aspartate repeat region protein SdR.
KW	Multicomponent vaccine; immunostimulatory; antibacterial; MSCRAMM; microbial surface components recognising adhesive matrix molecules; collagen binding protein; CBP; CNA; fibrinogen binding protein; clumping factor A; ClfA; ClfB; FibrB; fibronectin binding protein; Staphylococcus infection; serine-aspartate repeat region protein; SDR protein; SdR.
KW	serine-aspartate repeat region protein; SDR protein; SdR.
OS	Staphylococcus epidermidis.
XX	
FH	Key Location/Qualifiers
FT	Misc-difference 12 /note= "Encoded by in-frame stop codon TAA"
FT	Misc-difference 28 /note= "Encoded by in-frame stop codon TAA"
FT	Misc-difference 1771 /note= "Encoded by in-frame stop codon TAA"
FT	Misc-difference 1774 /note= "Encoded by in-frame stop codon TGA"
FT	Misc-difference 1793 /note= "Encoded by in-frame stop codon TGA"
FT	Misc-difference 1800 /note= "Encoded by in-frame stop codon TAA"
FT	Misc-difference 1800 /note= "Encoded by in-frame stop codon TGA"
XX	XX WO200012131-A1.
PX	WO200012131-A1.
PD	09-MAR-2000.
PF	31-AUG-1999; 99WO-US19727.

CC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
format directly from WIPO at
CC ftp://wipo.int/pub/published_pct_sequences.

XX Sequence 841 AA;

Query Match	Similarity	Score	DB	Length
Best Local Matches	14.8%; 158; Conservative	456; 27.1%	22; Pred. No. 9e-17;	841;
			Mismatches	222; Gaps 25;
Qy	42 GIERRSEDRTESTNVDENBRAFLOKTPDNTILTEEVKESSVES---SNNSIDTAQ	97		
Db	45 gheakaentngengsknett---apen-----kttkkvdsrqdkntqataad	92		
Qy	98 QPSHHTINRBEVSQVSDNYBDSHSDFANSKIKESNTESGKEENTIEQPNRKVEDSTSQ	157		
Db	93 qpkvt-----msdsatvketsnsmqs-----pqnatangsttk	125		
Qy	158 PSGYVINIDEK--ISNODELLNLPINEYEYKARPLSTTSQPSIK----RVTNOLAA-	208		
Db	126 tsnvtnkdkssttysnetdksnl-----tgakadvsttpkttikprtrlnrmavntvaap	179		
Qy	209 BQGSANVNLHLKVTD-QSITEGK-DDSEGVIK--RHDAEMLIYDTEFDDKVKSGDTWT	263		
Db	180 qgqtvnvdvkhfnsidialdkghvngttgttefwatsdvvikikanytiddsvkegdtf	239		
Qy	264 VDIDKNTVPSLTDSPFTIPKTKDNSEIATGTYDKNKQOTYFTDYVKKENKAHLK	323		
Db	240 fkygyfrpsvrqlsqsgtqlynaagnilaqkjyastnttttqytrqytrvgsfe	299		
Qy	324 LTSYIDKSKVPPNNNTKLDEVKTAASSVNKTIVVEORPNEFNANLQSMTNTDKNHT	383		
Db	300 qvafakrknattdktaykmevlgnatyseelivdy--gnkkaaplissnyinedls	356		
Qy	384 VEQTIVN-PYRSARETNV-NISANGDEESTTIBDSTIIRKVKYGDNONL---PDSN	436		
Db	357 rnmntayvnqpkntytkqtfvntl----gkfpnphaknfklyevtdqngfvdsrtptds	411		
Qy	437 RYIDSEYEDTNDYAQLGKNNDVINFGENIDS--PYIIVK-----SKVDPNRKDYT	489		
Db	412 kldvdqfd1---jsndkntatvdlmkgqtsnqyiqgqavpnsstdngkidy--	466		
Qy	490 IQTQTVNMQTTINBYEGERPTASYDNTIAFSTSSGOCOGDLPPEKTYKIGDYWEDVDKG	549		
Db	467 -----tldtdktykw---snlysnyngsclangd-----qkkylnlgdyvwedtnkdg	511		
Qy	550 IONTNDNEKPLSNVLVLTYPCTS-KSVRDPEDGKYQFDGV	590		
Db	512 kdqa--nekgjkgvyvilkdsngkeleldrttdengkyqftgl	551		

Search completed: July 30, 2002, 10:30:30
Job time: 100 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 30, 2002, 10:28:55 ; Search time 33.65 seconds

(without alignments)
430.442 Million cell updates/sec

Title: US-09-147-405-11
Perfect score: 3087
Sequence: 1 HHHHHIPSSDEEKNDVNNN.....SKSVRTEDEGKYQFDGVQVD 593

Scoring table: BLOSUM62

Gapov 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued,Patents_AA;*

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6: /cgn2_6/ptodata/2/1aa/bactfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	452	14.6	933	3 US-09-293-728-2	Sequence 2, Appl1
2	452	14.6	933	4 US-09-021-868-2	Sequence 2, Appl1
3	349	11.3	454	5 US-08-856-253-7	Sequence 7, Appl1
4	259.5	8.4	1112	2 US-09-714-403-2	Sequence 2, Appl1
5	259.5	8.4	1161	4 US-09-377-535-2	Sequence 2, Appl1
6	209	6.8	630	4 US-08-973-462-9	Sequence 9, Appl1
7	198	6.4	783	6 5231168-2	Patent No. 5231168
8	197	6.4	2314	4 US-09-268-347-49	Sequence 49, Appl1
9	196.5	6.4	1786	4 US-08-973-462-8	Sequence 8, Appl1
10	189.5	6.1	1664	2 US-08-642-846-2	Sequence 2, Appl1
11	189.5	6.1	1664	4 US-09-266-604-2	Sequence 2, Appl1
12	188.5	6.1	1435	2 US-08-568-459A-4	Sequence 4, Appl1
13	188.5	6.1	1435	2 US-08-487-8269-2	Sequence 4, Appl1
14	186.5	6.0	3111	2 US-08-460-309-4	Sequence 4, Appl1
15	185.5	6.0	3111	2 US-08-125-077-4	Sequence 4, Appl1
16	185	6.0	2048	4 US-09-288-347-48	Sequence 48, Appl1
17	184.5	6.0	2391	2 US-08-416-855A-2	Sequence 2, Appl1
18	184.5	6.0	2391	4 US-09-150-741-2	Sequence 2, Appl1
19	177.5	5.7	1087	1 US-266-002-5	Sequence 5, Appl1
20	176	5.7	3788	4 US-09-336-447A-76	Sequence 76, Appl1
21	175.5	5.7	1104	4 US-09-266-347-28	Sequence 28, Appl1
22	175.5	5.7	1104	4 US-09-266-347-34	Sequence 34, Appl1
23	175.5	5.7	1183	2 US-08-447-031A-2	Sequence 2, Appl1
24	175	5.7	1147	3 US-08-470-260-5	Sequence 3, Appl1
25	175	5.7	1147	3 US-08-477-491-5	Sequence 5, Appl1
26	175	5.7	1147	4 US-08-465-662-5	Sequence 2, Appl1
27	175	5.7	3289	2 US-08-477-451-2	Sequence 2, Appl1

ALIGNMENTS

RESULT	Query	Match	Score	DB	Length	Best Local Similarity	Pred. No.	Sequence
1	US-08-293-728-2	US-08-293-728-2	1	US-08-293-728D	933	26.6%	1	Sequence 1, Appl1
				Patent No. 6008341				GENERAL INFORMATION:
				APPLICANT: Foster, Timothy J.				APPLICANT: McDevitt, Damien L.
				FILE REFERENCE: 05344-105011				FILE REFERENCE: The S. aureus Fibrinogen Binding Protein Gene
				CURRENT APPLICATION NUMBER: US-08/293,728D				CURRENT FILING DATE: 1994-08-22
				NUMBER OF SEQ ID NOS: 20				NUMBER OF SEQ ID NOS: 20
				SOFTWARE: PatentIn Ver. 2.0				SOFTWARE: PatentIn Ver. 2.0
				SEQ ID NO: 2				SEQ ID NO: 2
				LENGTH: 933				LENGTH: 933
				TYPE: PRT				TYPE: PRT
				ORGANISM: Staphylococcus aureus				ORGANISM: Staphylococcus aureus
				US-08-293-728-2				US-08-293-728-2

Query Match 14.6%; Score 452; DB 3; Length 933;
Best Local Similarity 26.6%; Pred. No. 1 6e-18; Mismatches 234; Indels 86; Gaps 26;

Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;

Sequence 2, Appl1

Sequence 7, Appl1

Sequence 2, Appl1

Sequence 2, Appl1

Sequence 9, Appl1

Pattern No. 5231168

Db 92 NP-----AQEETQSNTAATTEETTEPTVIGTATTNTQANTPATQG-SNTNAEELVN- 143

Db 144 -QTSNETTFNNTV-----SSWNPSNSTNAENVSITQDSTERTPSN--NES 189

Db 190 APOSTDASKNDVNVQAVNTSPRMRAFSLAAVADAPAGTDITNQLTNVNGI-DSGTT 248

Db 249 VPIPHQAGYVVKLWGFYSVNSAVKGDFTEKITVPKELNLNGVTFKAVPPIMGD-QYLNG 307

Db 256 IKRDAENLIYDVFEDKVKGDMIVDTIDKNTVPSLDSFTPKIKNSGETATG 295

Db 296 TWDNKNIQITYTFDYYDKYENTKAHLKLTSDKSKVPPNNTKL-DVEYKTAASS-VN 352

Db 308 VIDS-DGNVIYFTDVKDVKATIMPAVID---PEVKKTSVNTLIGGTT 362

QY 353 KTTVKEVRQPNEERTAMQSMTNTDKRNHVEOTIYINPL--RYSAKETVNISNGE 410

Db 363 KTVLVDYEVKGKFYNLNSIRKTIDQIDRNTNTYRQITVNP SGDNTIAVLIGLNKLPTDS 422
 Qy 411 GSTLDDSTIKIVKVGNQNLPSNRIDYSEPDNTNDYAQGNNDNINFG--- 466
 Db 423 NALIDQOMTSIKYKVNDNADESYFV-NPENFEDTNTSNWTFPKNQVKVEFPDD 481
 Qy 467 NIDSPYIIVKVISKVDPN-KDVTIQQTVMTTINETYGE--FRTAASYDNTIAFSSTSG 523
 Db 482 QITTPYIVVNGHIDPNKGD-----LAURSTLYGNSNIWRSMSWDNEVAFNNGSG 534
 Qy 524 QSGQ-DLP--PEKTYKGDY--VWEDYDKD-GIONTN 556
 Db 535 SGDGIDPKVVPBOPDEGEIEBIPEDSDPGSDSGSDS 573
 RESULT 2 US-09-421-868-2
 ; Sequence 2, Application US/09421868
 ; Patent No. 6177084
 ; GENERAL INFORMATION:
 ; APPLICANT: Foster, Timothy J.
 ; APPLICANT: McDevitt, Damien L.
 ; TITLE OF INVENTION: The S. aureus Fibrinogen Binding Protein Gene
 ; FILE REFERENCE: 03344-105011
 ; CURRENT APPLICATION NUMBER: US/09/421, 868
 ; CURRENT FILING DATE: 1999-10-19
 ; PRIOR APPLICATION NUMBER: 08/293,728
 ; PRIOR FILING DATE: 1994-08-22
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 933
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-421-868-2
 Query Match Best Local Similarity 14.6%; Score 452; DB 4; Length 933;
 Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;
 Qy 8 SSDEEKMDVNNNQSINTDDNNQIKEETNNYDGEBKRSPDRTESTNVEAEATFLQ 67
 Db 51 SWESKSNDDSSVSAKPDDTNV-----SPDKISSNTN--NGETSVAQ 91
 Qy 68 TRODNTHLTEREVKESSVESSNSISDTAQOPSHTTINRESSVOTSPNVERSHVSFANS 127
 Db 92 NP-----AQQTQSSNTAETEPTVGTATTNQAPATQS-SWNAELVN- 143
 128 KIKESNTESKGKEENTIOPNKYKEDSTSQQSGYNTIDEKSINQDELIN-LPINEYENKA 186
 Db 144 -OTSNETTEENDNTNV-----SSVNSPONSTNAENVSTQDSTEATPSN--NES 189
 Qy 187 RPLSTTQAQPSKIKRVTVN-----QLAEBQGSNNYHLITVTDQ--STEGYDSEGV 235
 Db 190 APOSTDASNKDVNQAVNTSPRMRAESLAVAADAPAGIDTINQINVIGI-DSGT 248
 Qy 236 IKRHDAAENLIVYTFEYDVKVSGDTMVDIDKNTVPSDLUSET-PIKINSGELATG 295
 Db 249 VIFHQAGVVKLNGFSPVNSAVKGDTKIPKELNINGVSTAKVPPIMAGD-QYLANG 307
 Qy 296 TVDNKMKQITTFDVKYKENIKAHLKLTQIDKSKVNNTKL-DVEYKTALESS-VN 352
 Db 308 VIDS-DGNVITYFTDVTNPKDKVATLMPAYD---PEVVKGNVTLATGISTAN 362
 Qy 353 KUTVEQORPNERTANLQSMTNTIDKHNHVEQTYINPL--RYCAKETVNNSNGDE 410
 Db 363 KVVLVDYEVKGKFYNLNSIRKTIDQIDRNTNTYRQITVNP SGDNTIAVLIGLNKLPTDS 422
 Qy 411 GSTLDDSTIKIVKVGNQNLPSNRIDYSEPDNTNDYAQGNNDNINFG--- 466
 Db 423 NALIDQOMTSIKYKVNDNADESYFV-NPENFEDTNTSNWTFPKNQVKVEFPDD 481
 RESULT 3 US-08-556-253-7
 ; Sequence 7, Application US/08856253
 ; Patent No. 6288214
 ; GENERAL INFORMATION:
 ; APPLICANT: Hook, Magnus
 ; APPLICANT: Patti, Joseph M.
 ; APPLICANT: House-Pompeo, Karen
 ; APPLICANT: Sthanam, Narayana
 ; APPLICANT: Symersky, Jinrich
 ; TITLE OF INVENTION: COLLAGEN BINDING PROTEIN COMPOSITIONS
 ; TITLE OF INVENTION: AND METHODS OF USE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P.O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: U.S.
 ; ZIP: 77210
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/556,253
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/017,678
 FILING DATE: 16-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Kitchell, Barbara S.
 REGISTRATION NUMBER: 33,928
 REFERENCE DOCKET NUMBER: TAKM:193
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 471-7577
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 345 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 ; US-08-556-253-7
 Query Match Best Local Similarity 11.3%; Score 349; DB 4; Length 345;
 Matches 102; Conservative 61; Mismatches 136; Indels 32; Gaps 15;
 Qy 220 VTDOO--SITEGYDDESGVVKHADENLIVYDVTEDDKVKGDTMVDIDKNTVPSDLTD 277
 Db 25 ITNQLNTVTVGI-DSCTTVYFHQAGVVKLNGFSPVNSAVKGDTKITVKEELNLNGVTS 83
 Qy 278 SFTIPKIKDNSEGETIATGTYVNNKQIYTTFDVKYKENIKAHLKLTQIDKSKVNN 337
 Db 84 TAKVPPIMAGD-QYLANGVIDS-DGNVITYFTDVKYKDDVKATLMPAYD---PEV 137
 Qy 338 TKL-DVEYKTALESS-WNKTTIVEORPNERTANLQSMFNTIDKHNHVEQTYINPL- 393
 Db 138 KRTGNTVTLATGIGSTANKVLUDEVYKGYKYNLJIKTIDQIKNTTROTIVNPMSG 197

Db 279 -----TSISNEFKSTIGCQEQITKGTVNLGVNLYNESTKESNYTNGLSNVGGIESYNT 331
 Qy 381 NHTVEQTIVINPLRSAKETNVIISNG-----DEGSTIIDSTIKVYKDNO 430
 Db 332 TGFEEWVWVYVNPNRNTIPTAMNLWGFGRARSNTSDLENDANNSAELGEIQVYEVPE 391
 Qy 431 NLPDSNRKYDSEVEDT----NDDYAQLGNNDV---INTNFGN--IDSPTYIKVSK 479
 Db 392 KUBSSYGV-----DTYKLURTDIFAGLNGFQMTKRQRIDFGNNIQNAFIKIVTGK 444
 Qy 480 YDNKKDDYTIIQVTMOTTNEYTGERPAS-----YDNTIAFSTS:SGOGG--- 527
 Db 445 TDSS-----GKPLVQVNSLASFRGASEYRAAFTPVGNNVYFONEALSPKGSGSKSE 497
 Qy 528 -----DLRPEKTYKIGDVWEDVDKGQONTUNEKPLSNVNLTVPGTISKVR-TDE 581
 Db 498 FTKPSITVANLKRVAQIRFKMSTDNY-----PLPEAEFLRSSNGNSQLEASNT 549
 Qy 582 DGKVQF 587
 :
 550 QGEVHF 555

RESULT 6

US-08-973-462-9
 ; Sequence 9, Application US/08973462B
 ; Patent No. 6191270
 ; GENERAL INFORMATION:
 ; APPLICANT: DROUHIE, PIERRE
 ; APPLICANT: DAUBERSES, PIERRE
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
 ; FILE REFERENCE: 0660-0125-0 PCT
 ; CURRENT FILING DATE: US/08/973, 462B
 ; EARLIER APPLICATION NUMBER: PCT/FR96/00894
 ; EARLIER FILING DATE: 1996-06-12
 ; EARLIER APPLICATION NUMBER: FR 95/07007
 ; EARLIER FILING DATE: 1995-06-13
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO: 9
 ; LENGTH: 630
 ; TYPE: PRP
 ; FEATURE: ORGANISM: Artificial sequence
 ; OTHER INFORMATION: Description of Artificial Sequence:Polypeptide
 ; US-08-973-462-9

Query Match 6.8%: Score 209; DB 4; Length 630;
 Best Local Similarity 19.5%; Pred. No. 8.6e-05; Matches 116; Conservative 121; Mismatches 206; Indels 152; Gaps 28;

Db 9 SDEEKHDVNN-----NOSINTDDNQNQTIKKETTNNDGIERSEDRTEST- 54
 Db 59 SDELFNELLNSVNGEKEVKENILESQVNDDIFNSLKVSQEQQHNVEEVEND 118
 Qy 55 -----TIVDENE-----ATFLOK-----TPODTHJTEEEK 81
 Db 119 EBSVERVNEVNEENDGSVASSVSIASSVSDIDESSTSSTEENVAPTVTIVAPVVEETV 178
 Qy 82 ESSYESSNSSIDAQPSHTTINREFSYOTSDNVEDS--HVSDPANSKIKES--NTE 135
 Db 179 AFSVVSVSVAPSVEEVAPS-----VEESV-AENYEVESVANEVIVEVAPSV 231
 Qy 136 SGKEETIEPPNKVHDSTQSOPSSYTNIIDEKIS NQDELLNLPINE----YENKARPL 189
 Db 232 ESSVAENVEESAVENTEESVRE-----NVEEVSAENVEELVAFVEEVAPTVIEVAPT 285
 Qy 190 SITSQAPSICKVTVQMLAAEGGSNNVNLKIVTQDOSITEGYDSDSBCVIKAHDAAENLYDVT 249
 Db 286 VEESTAPTVPEEVIVVSVSVSVAPS-----EBSVAENVEESV-----AENVEESVA 331

RESULT 7

5231168-2

Patent No. 5231168
 ; APPLICANT: DZIEGIEL, MORTEN; BORRE, MARTIN; JEPSEN, SØREN;
 ; VUUST, JENS; RIEDECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PALLE H.
 ; TITLE OF INVENTION: MALARIA ANTIGEN .
 ; NUMBER OF SEQUENCES: 19
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: 05/074409, 658
 ; FILING DATE: 18-SEP-1989
 ; SEQ ID NO:2:
 ; LENGTH: 783
 ; 5231168-2

Query Match 6.4%: Score 198; DB 6; Length 783;
 Best Local Similarity 18.5%; Pred. No. 0.0009; Matches 118; Conservative 127; Mismatches 216; Indels 176; Gaps 28;

Db 4 HHHPSSSDEEKDVINNNQINTD-----DNNQIINK-----EETNNYDG 42
 Db 54 HHENESSEVSNSSELNEENFESDKSVTPEAPEEVSEESNPEAENEESIEAHQEELI 113
 Qy 43 IERKRDRTTESTNVDNEATFLQKT---PODTHLITEEVKSSSVSESSNSIDAO 97
 Db 114 VPEQDDESEGESGLYDNEEGDFPEEPHEEFEPDON---DSELSLENELVESKVSPEA 169
 Qy 98 QPSHTINREESV-OTSNDNEDSHVSDFANSKIKESNTESGKEENTIEQPNVKEDTS 156
 Db 170 ---HVEIVSKVSPPAERVE--IVSEKSSTSEPA-EHVESEOSN-NEPSEKGDGPVPS 222
 Qy 157 QPSGTNIDKEISNODDELLNLPINRYE-NKARPLSTTSAQPSIKRVTVNOLAQSGSYN 215
 Db 223 KP--FEETI EKVDPVPKIVDQIPELPNFVDSQNPQEPVPEPSF--VKIERVPSENKHAS 277
 Qy 216 HLKIVTDOSITEGYDSEGVYKADAEILYDVFEVDKVKSGDTMTWDIDKIVVPSDL 275
 Db 278 -----VDEPEKEKENVSEVVEEKONSQESVEEIPVN-EDBEFDVHTEQDLDHRTDPEI 331
 Qy 276 TDSFIIKKDKNSGBIIATGYDKNKNQITYFTDVYKVENIKAHLKTSYIDSKVFN 335
 Db 332 VEVEIPS-----VVEEVPEEV-----EJHENEVAHPEVIEVFPBP 362
 Qy 336 NNTKLVDVEKTALESVNTKTTVEVQRPNE-NRTANLQSMPTN-----DTKNVTEAT 388
 Db 363 QNN-----EEQINEDDKSAHQIHEIVEFELIPDDEKNEKEHEI 403
 Qy 389 YINPLRSAKETNYNISNGDEGSTIIDSTIKVYKGDQNLPDSR---IYDYSEY 444
 Db 404 -----VEVEELPEDIKEKEQHEIVEET----LPEDKNEKEVHEIVEV 445
 Qy 445 EDVNTDDYQOLGNNDVNVNFGNIDSPVPIKVISKYDPNKKDDYTIIQVTMOTTINSET 504

Db 446 EILPEDKNEKGQHEIVEVEE-----EILPEDKNEKGQHEIVEVEE----- 493
 Qy 505 GEFRTASYDNTIAFSTSSGQGQGD-----LPPEKYKQGDYVWEDVVKIGQIQTNDNE 557
 Db 494 -----KGQHEIVEVEE-----EILPEDKNEKGQHEIVEVEE----- 531
 Qy 558 KPLSNYL-VTLYPDTSKSVRTDEQKDYDGVQD 593
 Db 532 KGQHEIVEVEE-----EILPEDKNEKGQHEIVEVEE 561

RESULT 8 |
 US-09-268-347-49
 Sequence 49, Application US/09268347
 ; Patent No. 6335182
 ; GENERAL INFORMATION:
 ; APPLICANT: Loosmore, Sheena M.
 ; TITLE OF INVENTION: RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS
 FILE REFERENCE: 1038-860
 CURRENT APPLICATION NUMBER: US/09/268, 347
 CURRENT FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 49
 LENGTH: 2314
 TYPE: PRT
 ORGANISM: Haemophilus influenzae
 ; US-09-268-347-49

Query Match 6.4%; Score 197; DB 4; Length 2314;
 Best Local Similarity 21.1%; Pred. No. 0.0022; Matches 135; Conservative 101; Mismatches 261; Indels 144; Gaps 30;
 Qy 11 ERKDNDVNNQNSIN-TDNQNIKEETNMYGIEKSEDRRESTTNVDEATFLOKTP 69
 Db 379 ERQADKLTDNNNIGVWVDNTNTLKVKLAKNLUGLE-----AVSTKNITASE---KVT 428
 Qy 70 QDNTHLTEEVKRESSYESSNSNSIDTAQPSHTINRRESVQSDN---VEDSHVSDFA 125
 Db 429 GSGNNNTAAELQSGGLTFPTTNASTD-----KTVGTDGLKFTDNNTAEDT--IRIT 479
 Qy 126 NSTIKESWESKEGREENTEQP---NKYKEDDTTSOPSGYTNIDEKIS-NQDELNLPINE 181
 Db 480 KOKIGFSNKKAGTYDEN--KPYLDKDKLKGNSTLNNQGLV-UNNTIGGSNQIQV--- 531
 Qy 182 YENKARPLITSQAQSPSKRRTVNQLAEGGSNVNHLIKVQD SITE--GYDSEGVIKA 238
 .o. 532 -----GADGKRFADV-----VNVSAAKFGTRIPEBIFGADAGKVK 572
 Qy 239 H----DAENL-IVDVFEDVKVKGDMTMVDDKNTVPSDLDSFTIPKIK---DNNG 289
 Db 573 KSYFLDKKKQLQVGVKITKDGSGINAGDOOKISINVKDAD-----DODAVYKQLQVQDADG 629
 Qy 290 EIXATGTYDVKNQIOT---YTYTDYVQYENT---KAKHLKTTSYDKSKVNNPL 341
 Db 630 ALOSFSTREDKOGEFTISLYNSMNTPNFETITFAGENGISISNDTRKGV---KVG 684
 Qy 342 VEKTALSSVNUKITVEYORPNENRANLQSMTNIDMKHNHTVEQTYINPLRSAKETN 401
 Db 685 IDPENGLPTPKLV-----GSDKGDKHQLVIEQASNGTKNTIRGWSPTLSI-TN 735
 Qy 402 VNISGNGDGGSTIIDSTIKVKGDMON---PDSSRIVDYESEBVNTDYAOLG 456
 Db 736 AGGVRTTROGNTTSDERKSKAASIGDILNTGFNLKNNNSNSVCFVSTVTVDFD---G 791
 Qy 457 NNNDVNINGNGNISPYIIRKVISQDPNQDYT-----IQTQVTHQTTMEY 503
 Db 792 NATTAKVYIDETNOTSKY---TYDVNVDEKTEILTGDNGKTN:GVKTTLTNTANGK 847
 Qy 504 TGEERTASD-----WIAFSISSGGQGQDPEPEKYYI-GDYWED---WD 546

RESULT 9 |
 US-08-973-462-8
 Sequence 8, Application US/08973462B
 ; Patent No. 6131270
 ; GENERAL INFORMATION:
 ; APPLICANT: DRUILHE, PIERRE
 ; APPLICANT: DAUBERSIES, PIERRE
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
 FILE REFERENCE: 060-0125-0 PCT
 CURRENT APPLICATION NUMBER: US/08/973, 462B
 CURRENT FILING DATE: 1998-02-05
 EARLIER APPLICATION NUMBER: PCT/FR96/00894
 EARLIER FILING DATE: 1996-06-12
 EARLIER APPLICATION NUMBER: FR 95/07007
 EARLIER FILING DATE: 1995-06-13
 NUMBER OF SEQ ID NOS: 29
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 8
 LENGTH: 1786
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: polypeptide
 ; US-08-973-462-8

Query Match 6.4%; Score 196.5; DB 4; Length 1786;
 Best Local Similarity 18.7%; Pred. No. 0.0017; Matches 128; Conservative 142; Mismatches 264; Indels 149; Gaps 26;
 Qy 21 QSINTDNDQNIKEETNMYGIEKSEDRRESTTNVDEATFLOKTPDQTHAEEV 80
 Db 549 ESVEENVEESAENVEESAENVEESAENVEE-----SVAENVEEIVAPTEEVAPVVEI 606
 Qy 81 KESSVSESSNSSTDATQPSHTINRRESVQSDNVDSDHVSDFANSKIKSNTSEGKE- 139
 Db 607 VAPSVEVAPSVEE-----NVESV-AENVES-----VAENVEESAENVEE 654
 Qy 140 -----ENTIEQ---PNKYKEDDTTSOPSGYTNIDEKIS-NQDELNLPINEKA 186
 Db 655 VAPTEEVAPTEEVAPSVEVSVSVEEVEEVEEVEEVEEVEEVEEVEEVEA 712
 Qy 187 RP-STSQ-----PSIKRV-----TVMOLAJAEBOGSNNHLKRTDOSITEYDDSGV 236
 Db 713 ENVEEESAENVEEIVAPTEEVAPTEEVAP-----SVVESVAPSVESVEEVEEVE 767
 Qy 237 KAIDAENLYDVFEVDVKVKG-----DTMVVDIDKNTVPSDLDSFTIPKIKNSGETAT 294
 .o. 768 -----AENVEEESAENVEEESVAPTEEVAPS-----VEESVAPSVESVEEVEA 821
 Qy 295 GTVDNKNQI-----TYTFDYV-DKYNIKAHLKTSYDKSKVPPNNTKLDVKEVTL 348
 Db 822 NLSDNLNSLNLGGIETEEIKDSLNEIEKEVKNVTT-----ILNVEEETAEVSYTE 874
 Qy 349 SSV-----NRTTVEYOPENRATNQSMFNMIDN----- 381
 Db 875 SNILEIQTNTNDTIEKLELHENLVAALENTQSEEKEVIVDVEEVEEWTI 934
 Qy 382 -HIVEQ-----TIVINPLRYSAKETNVTNSGNGDSEGSTTIDSPSIKYKVGNQ 431
 Db 935 IETVEAEEBSAANTTEIFENLENBENAVESNENYALNLEKNETVNFVLDKVEETVLSG 994
 Qy 432 LPDSNRIDYSEEDVNTDNYAOLGNNMDVINGNIDSPYIIRKVISQDPNQDYT- 490
 Db 995 ESLENEMDKAFFSEF--DNVKGQIQLNLTGMFRSIEUTSIVOSEEVKDLVNNVSSL 1052

Query 491 - QOTVIMOTTINETYGEFRASASYNTIAFSTSSG--- 523
Db 1053 DNIEENMKEGLLNKLNSSTEYGVOETVTEHVQNVYDVDPAMKDOFLGLINNEAGGLKE 1112
Qy 524 - OGGDLPPEPKTYKGDDWEDVKDGQTNTDIEKPLSNUVL---VLT 568
Db 1113 MFFNLEDVFKSSESDVITEIK-DEPVQEVREKETVSIEEEMENTIVDYLEEEKEDLTDK 1171
Qy 569 YPDCTSKSYRTDEGKQFDGWQ 591
Db 1172 MTAVERSIEISSLKEETESTIK 1194

RESULT 10

US 08-642-846-2 Application US/08642846
; Sequence 2, Application US/08642846
; Patent No. 5886151
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDL, CATHERINE M.
; APPLICANT: TAO, NIAN JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBicans GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/642,846
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00280101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 1664 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-642-846-2

Query Match 6.1%; Score 189.5; DB 2; Length 1664;
Best Local Similarity 20.4%; Pred. No. 0.0039;
Matches 131; Conservative 105; Mismatches 236; Indels 171; Gaps 31;

Qy 15 DVINNNQS---INTDDNNQITKK-----EETNNYDGIEKRSDRDTST 55
Db 138 DKVWENHAPTYINTSPNKSIMKKATPKASPCKVAFVTPNPELHYP---DNRBEEEDSQQ 195
Qy 56 NVDNEATEFLQKUPQDNTHLTBERVKESSSVSSNSSIDAQPSHTP----INREE 108
Db 196 KEDSVEPPLIQ----HOWKDPSQFNYSDEDDINASVPPTP-PFLHTTKPTAQLLNRR 247
Qy 109 SVQTSNDVSDHSVD----PANSKKE----SNTESKEENIEQPKVKVEDST 155

RESULT 11

US-09-264-604-2 Application US/09264604
; Sequence 2, Application US/09264604
; Patent No. 6344411
; GENERAL INFORMATION:
; APPLICANT: HOSTETTER, MARGARET K.
; APPLICANT: GALE, CHERYL A.
; APPLICANT: BENDL, CATHERINE M.
; APPLICANT: TAO, NIAN JUN
; APPLICANT: KENDRICK, KATHLEEN
; TITLE OF INVENTION: CANDIDA ALBicans GENE, INTEGRIN-LIKE
; TITLE OF INVENTION: PROTEIN, ANTIBODIES, AND METHODS OF USE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MUETING, RAASCH, GEBHARDT & SCHWAPPACH, P.A.
; STREET: 119 NORTH FOURTH STREET, SUITE 203
; CITY: MINNEAPOLIS
; STATE: MINNESOTA
; COUNTRY: USA
; ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/264,604
FILING DATE:
CLASSIFICATION:
PRIMER APPLICATION DATA:
APPLICATION NUMBER: US 08/642,846
FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.00280101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217

Db 248 EV---NSEPEALTDMLKRENFSNLSDLERKVNLSPNNNNKNVSDMDSHLQ---N 299
Qy 156 SOPSGBTIDEKIKNQDELLNIPINEVENKARPL-STTAQPSIKRTVNOLAEGSNV 214
Db 300 LQDASKKTTNEINHLSFALKAPKDNE--PLNSUTNADSLRSRGSSQSLQSLRND 356
Qy 2115 NHLIKV---TDOSITEYYDSRGVKAHAENLIYDVTFEVDDKVKGDTMTVIDKNTV 271
Db 357 NRVLESVFGSPKVNPGSLNDGIGFKSD---EVVESL 392
Qy 272 PSDLT-DSFTIPKIKD---NSGEIATGTYDNKNKOCITYFTDVKYENIKAH--- 321
Db 393 PROLSRKLETTEREHDAPEHNNEFIDAKSTNTNKG-OOLVYSSDDHLDIFDKSYNTHQS 451
Qy 322 -LKTSVTDKSKVPPN-----NTKIDVEKTALSSVX 353
Db 452 IINLLNSASQSOISLNALEKOROTOCOQTOAEPEEETSESDNIVKQEPKSNLERYKV 511
Db 512 TIKKEPSSATEIKAPKRFSSKILRKNEDEAEPADIPPKNEANSHVETDALLKA 571
Qy 407 -NGDEGSTIDTIDTIIK-YKGVDNQDLSRDIYDSEYEDVNTDQAOLGN---NDV 461
Db 572 LNDEDESSTQTSKMSRHFDSWKLDESDN---GDREI---NDDISREFKSDINDV 625
Qy 462 N-----INFNIDSYIYKISKDPPKDNYTTOQTVIMOTTINETYGER---T 509
Db 626 SOTSDIIGDKYGNISSETTAKTLA---PPRSNDNKENKSLESDPANNESLQQOLEVPHT 682
Qy 510 ASYDNTIAFSTSSQGOGDLPPEK---TYKGDY-WVEDVK 547
Db 683 KEDDSLILANSSNIA----PPEELTUPVVEANDYSSENDVTK 719

TELEFAX: 612-305-1228
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1664 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: protein

US-09-264-604-2

Query Match

6.1%; Score 189.5; DB 4; Length 1664;

Best Local Similarity 20.4%; Pred. No. 0.0039; Matches 131; Conservative 105; Mismatches 236; Indels 171; Gaps 31;

QY 15 DVINNNQG--INTDDNNQIKK-----EETNNIDGIERSEDRTEST 55
 Db 138 DKVNNENHAPTYINTNSNKIMKKAPKASPRKVAFTVNPETHTP--DNEVEEQSQO 195
 QY 56 NVDENERATFLOKTPQDNTHLIEEVKESSVESSNSNSIDTAQQPSHT----INREE 108
 .D 196 KEDSVEPPLIQ----HOWKDPSONYSDEDTNAVASVPPP-PPLHITKPFQAQLNKN 247

QY 109 SVQTSDVNEDHSVSD-----FANSKIKE----SNTESGKEENTIEQPBNKVKEDST 155
 Db 248 EV----NSEPARLTDMKLKRENNNLNSDPTNNNSKVNDSMDHLSQ----N 299

QY 156 SOPSGYTNIDEKISNOELLNPEVENEVKARPL--STSAAOPSISKRTVNOLAEQGSNV 214
 Db 300 LQDASKRKTNEHNILSFALKAPKNDIEN--PLNSLTNAISLRSSGSSQSLSLRND 356

Qy 215 NHLIKV--TPO SITEGYYDSEGVKAHDENLIVDTFEVDDKVKGDTMVIDKNTV 271
 Oy 357 NRVLESVPGSPKKVNPGLSLNDGIGKGFSD-----EVVESLL 392

QY 272 PSDLT-DSFTIPKIKD----NSEGETATGTYDNKNNQKITYTFTDVVKYENIKAH--- 321
 Db 393 PRDLRSKLTTRKEDAPEHNNEFIDAKSTNNKNG-QOLLYSSDDHLDSEFORSYNTEQS 451

QY 322 -LKLTSVSKRKPVPN-----NKLDEVEKTLASSVNK 353
 Db 452 IUNLNSASQOSISLNALEKQRTQEQTOAEEPEETPSDNTKVOEPKSNLEFVVK 511

QY 354 TITVEYORPNENTANLQSMFTNIDTKNH-TVEQTYINVPLRVSAKETVNNTSG---- 406
 Db 512 TIKKEPVSATEIKAKPKRFSSKLIRKNEDEIAEPADIHPKKENAANSHVETDALLKA 571

..QY 407 -NQDEGSPILLDISTLKV-YKVGDNQNLPSURRIYDVSEYEVNTDDYAQQLGN--NDV 461
 b 572 LNDEESEDTTONSTKMSRFHIDSWDWKLEDSND---GDRED--NDDTSRFERDSLNDV 625

QY 462 N----INFGNDSPIVIKVISKYDNPKDYTITQTVTMQTTINBYTGFER----T 509
 Db 626 SQSDSILGDKYNSSETTKIA--PPRSNDNKENSKSLEDFANNESLQQLEVHT 682

QY 510 ASYDNTAFTSSGQGQGDLPPEK---TYKGDY-WVEDVIR 547
 Db 683 KEDSILANNSNIA-----PPEELTIPVVEANDYSSENDVTK 719

RESULT 12
 US-08-568-459A-4
 ; Sequence 4, Application US/08568459A
 ; Patent No. 5849306
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chitnis, Chetan
 ; APPLICANT: Miller, Louis H.
 ; APPLICANT: Peterson, David S.
 ; APPLICANT: Su, Xin-zhuan
 ; APPLICANT: Wellens, Thomas E.
 ; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
 ; TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe Martens Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: California
 COUNTRY: US
 ZIP: 92660

COMPUTER READABLE FORM:
 COMPUTER TYPE: Flopy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION NUMBER: US/08/568,459A
 FILING DATE: 07-DEC-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Jersalem, Ned
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: NIH121.001CPL
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 235-8850

TELEFAX: (619) 235-0176
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1435 amino acids
 TYPE: amino acid
 STRANDEDNESS: single

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Plasmodium falciparum

US-08-568-459A-4

Query Match

6.1%; Score 188.5; DB 2; Length 1435;
 Best Local Similarity 20.5%; Pred. No. 0.0037; Matches 114; Conservative 102; Mismatches 199; Indels 141; Gaps 28;

QY 8 SSDEEKUDVINNNQINNDNNQIITKKEETNNVYDG----IEKASREDREESTANDEN 60
 Db 875 NSDEESEETVVNH-----ISKSPSINNGDDSGSGSATVSESSSSNTGLSIDDNN 923

QY 61 EAFLQQTIPQDMTHLTFEEV--KESSVESSNSNSIDPAQQSHTTNRSESVQTSNDV 118
 Db 924 GDTFVRTDANT---EDVIRKENADKDEDEKGADERHSTSSESLSSEPERKMLTDNEG 979

QY 119 SHVSDFANSKIKE--SNTESGKEENTIEQPBNKVK--DSTSOPSGTNIDE---- 166
 Db 980 NSLN--HEEVKEHTNSNDVQSGGTIVNNMTEKEKLDTLENPS--SSLDEGKAHELSE 1034

QY 167 -KISNQDNLNPINPEYENKARLSTSIAQPSIKRTVNQLAEQGSNNVHLIKVTDQI 225
 Db 1035 PNLSDDQDMNSNTP----GQLDNTS-EETERISNNERYKNE----REBRTL 1077

QY 226 TEYDDESGVIRAH-----DAENLYDVTFEVDDKVKGDTMTVDIKRTVPSDLDFE 279
 Db 1078 TKYEDI--VVKSHMNRESDDGE-LYD-----ENSLSTVNDSEDEAKMGD 1124

QY 280 TIPKIKDNGEITATGTYDNKNNQKITYTFTDVVKYENIKAHKLYTIDSKVPPNNT 339
 Db 1125 T-SEMSPNSHOITESDQDKNDMKTVGDLTGHVON----EISYPVGEIDEKLERESKE 1179

QY 340 LDVEYKTAASSVAKTIVTVEORNNENRANLQSM--FTNDQKNTVHQEQTINIPRVA 397
 Db 1180 IHRAEERLSTD--IHKINP-EDRNSTUHLKDRNEERHLTNQNINISQRDQ 1234

QY 398 K----ETNNIISNGDEGSTIDSTIKVYKVQGDQNLQEDPSNRIYDVSEYEVNTDDYQ 454
 Db 1235 KHGPHTMMNLHGPG----VSERSQINHSHQNQD----R 1266

QY 455 LGNNNDV----NINFGNIDSPYIIVKISKD-----PNKDDYTIOQVTMOTTI 500
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1267 GGNNSGNVLNMRNNNNFNNIPSRV----NLVDKKLDLDDYENRNDST-KELIKKLAEI 1320
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 QY 501 NEYGEFRFTASYDTNI 516
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1321 NKCNEISVKYCDHMI 1336
 | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 RESULT 13
 ; Sequence 4, Application US/08487826B
 ; Patent No. 599327
 ; GENERAL INFORMATION:
 ; APPLICANT: Sim, Kim L.
 ; APPLICANT: Chittnis, Chetan
 ; APPLICANT: Miller, Louis H.
 ; APPLICANT: Peterson, David S.
 ; APPLICANT: Su, Xin-zhuan
 ; APPLICANT: Wellens, Thomas E.
 ; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX AND PLASMODIUM FALCIPARUM ERTHROCYTE BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 45
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Knobbe Martens Olson & Bear
 ; STREET: 620 Newport Center Drive 16th Floor
 ; CITY: Newport Beach
 ; STATE: California
 ; COUNTRY: US
 ; ZIP: 92660
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/487,826B
 ; FILING DATE: 10-SEP-1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Israeli, Ned
 ; REGISTRATION NUMBER: 29,655
 ; TELECOMMUNICATION INFORMATION:
 ; REFERENCE/DOCKET NUMBER: NIH121.001CPI
 ; TELEPHONE: (619) 235-8550
 ; TELEFAX: (619) 235-0176
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1435 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Plasmodium falciparum
 ; US-08-487-826B-4

RESULT 14
 ; Sequence 4, Application US/08460309
 ; Patent No. 5834946
 ; GENERAL INFORMATION:
 ; APPLICANT: Engvall, Eva
 ; APPLICANT: Ilmo, Ilmo
 ; TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell and Flores
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,309
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/125,077
 ; FILING DATE: 22-SEP-1993
 ; APPLICATION NUMBER: US PCT/US 94/10730
 ; FILING DATE: 21-SEP-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/472,319
 ; FILING DATE: 30-JAN-1990
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/919,951
 ; FILING DATE: 27-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Kathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-LA 9721
 ; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-460-309-4

Query Match 6.0% Score 186.5: DB 2; Length 3111;
 Best Local Similarity 19.9%; Pred. No. 0.013; Gaps 32;
 Matches 142; Conservative 102; Mismatches 256; Indels 215; Gaps 32;

QY 28 NNQI~~K~~KEET----NN~~D~~~~G~~~~I~~~~E~~~~K~~~~R~~~~S~~~~D~~~~R~~~~T~~~~E~~~~S~~~~T~~~~N~~~~D~~~~E~~~~A~~~~T~~~~F~~~~L~~~~Q~~~~K~~~~T~~~~F~~~~D~~~~N~~~~H~~~~T~~~~I~~~~E~~ 78
 Db 1694 NEKA~~I~~~~N~~~~E~~~~T~~~~G~~~~R~~~~D~~~~E~~~~F~~~~R~~~~N~~~~E~~~~G~~~~L~~~~Q~~~~K~~~~-----EIDOMIKELRKRNLETOKAED 1743~~

QY 79 EYK~~S~~~~V~~~~E~~~~S~~~~S~~~~N~~~~S~~~~I~~~~D~~~~T~~~~A~~~~Q~~~~P~~~~S~~~~H~~~~T~~~~T~~~~I~~~~---~~~~R~~~~E~~~~E~~~~S~~~~V~~~~O~~~~T~~~~S~~~~D~~~~N~~~~V~~~~E~~~~D~~~~-HVSDFANSKIRESN- 133~~

1744 ELVAEA~~L~~~~K~~~~V~~~~K~~~~L~~~~G~~~~E~~~~S~~~~R~~~~G~~~~E~~~~N~~~~E~~~~M~~~~K~~~~D~~~~R~~~~E~~~~K~~~~Y~~~~N~~~~V~~~~D~~~~A~~~~W~~~~D~~~~L~~~~R~~~~E~~~~A~~~~T~~~~D~~~~K~~~~I~~~~R~~~~A~~~~N~~~~R~~ 1803

QY 134 -----TESKE--ENTIOPNKV-----KEDSTS 156
 1804 LFAVNOKNM~~T~~~~A~~~~L~~~~K~~~~K~~~~E~~~~A~~~~V~~~~E~~~~S~~~~G~~~~K~~~~R~~~~Q~~~~E~~~~N~~~~T~~~~L~~~~K~~~~E~~~~G~~~~N~~~~D~~~~I~~~~L~~~~R~~~~T~~~~Y~~~~D~~~~I~~~~Q~~~~T~~~~K~~~~1~~ 1863

QY 157 QPSGYTN~~I~~~~E~~~~K~~~~I~~~~S~~~~N~~~~-----QDELLNLPINEENKARPLISTSA---QPSIKRVVNQL 206~~

Db 1864 LPPMS~~E~~~~N~~~~D~~~~K~~~~D~~~~L~~~~S~~~~Q~~~~E~~~~I~~~~K~~~~L~~~~A~~~~E~~~~V~~~~S~~~~Q~~~~A~~~~E~~~~H~~~~Q~~~~A~~~~N~~~~D~~~~S~~~~A~~~~V~~~~L~~~~G~~~~I~~~~D~~~~K~~~~-----SFRNAT 1923~~

QY 207 AAEQG-SVNVHLIKVTDOSITEGYDSEGVIKAHDENLYIVTIEVDVKYRGDTMTVD 265

Db 1924 AAFKAYSN~~I~~~~K~~~~Y~~~~-----DRAEKVAK--EAKDLAHEAT----KLATGPR--G 1962~~

QY 266 IDKNTVPSLTSFTI-----PKNDNSEIATGT----YDNKNQI~~T~~~~Y~~~~F~~~~D~~~~Y~~~~V~~~~D~~~~3~~ 313

Db 1963 LKKEDAKGCLOSKSFRILNEAKKLANDKVENDEDHNGLKTRIENALARNGDARNGDILRTNLDTLG 2022

QY 314 KYENI--KAHLKLTSYIDSKVPPNNTK-----LDEYKTA~~L~~~~S~~~~V~~~~N~~~~K~~~~T~~~~I~~~~T~~~~3~~ 356

Db 2023 KLSAIPND~~T~~~~A~~~~K~~~~Q~~~~D~~~~K~~~~A~~~~R~~~~Q~~~~Q~~~~-----LDAQTELHONLDGLKKYKLADSAVKTNA 2082~~

QY 357 VEYQPNENR-TANLQSMFTNID-----TKNH~~V~~~~E~~~~Q~~~~T~~~~I~~~~N~~~~P~~~~R~~~~Y~~~~3~~ 396

Db 2083 V-VKDS~~K~~~~N~~~~K~~~~I~~~~D~~~~A~~~~T~~~~V~~~~K~~~~N~~~~Q~~~~E~~~~A~~~~R~~~~L~~~~I~~~~K~~~~P~~~~I~~~~K~~~~E~~~~L~~~~N~~~~K~~~~N~~~~I~~~~E~~~~K~~~~L~~~~I~~~~N~~~~A~~~~R~~~~Q~~~~K~~ 2141

QY 397 AKETN~~V~~~~I~~~~N~~~~G~~~~N~~~~-----EGS-----TIDDE~~N~~~~I~~~~K~~~~V~~<-----YK 425~~

3 2142 ANSIKVSVSSGGDCIRTYKEIKKG~~S~~~~N~~~~I~~~~N~~~~V~~~~N~~~~K~~~~T~~~~A~~~~V~~~~D~~~~N~~~~L~~~~I~~~~F~~~~C~~~~A~~~~T~~~~E~~~~M~~~~R~~ 2201

QY 426 VGDQNQ~~L~~~~P~~~~S~~~~N~~~~R~~~~I~~~~D~~~~Y~~~~S~~~~E~~~~V~~~~D~~~~Y~~~~N~~~~D~~~~Y~~~~4~~ 478

Db 2202 KGKVSEFLWDVEGGVGR~~E~~~~P~~~~D~~~~I~~~~D~~~~D~~~~S~~~~W~~~~Y~~~~W~~~~R~~~~A~~~~R~~~~G~~~~R~~~~N~~~~T~~~~S~~~~V~~~~-A~~~~D~~~~G~~~~P~~~~K~~~~A~~~~S~~~~T~~~~V~~~~2~~ 2259

QY 479 -KYDPN~~K~~~~D~~~~Y~~~~T~~~~T~~~~Q~~~~Q~~~~T~~~~W~~~~M~~~~Q~~~~T~~~~I~~~~N~~~~E~~~~Y~~~~G~~~~F~~~~R~~~~T~~~~A~~~~S~~~~T~~~~S~~~~5~~ 57

Db 2260 TH~~I~~~~H~~~~S~~~~T~~~~S~~~~P~~~~G~~~~T~~~~I~~~~L~~~~D~~~~V~~~~A~~~~N~~~~A~~~~M~~~~L~~~~F~~~~V~~~~G~~~~G~~~~T~~~~K~~~~L~~~~K~~~~A~~~~D~~~~A~~~~V~~~~R~~~~I~~~~T~~~~F~~~~G~~~~C~~~~M~~~~G~~~~T~~~~Y~~~~F~~~~D~~~~N~~~~K~~~~P~~~~-----I 2314~~

QY 538 G~~Y~~~~W~~~~V~~~~E~~~~D~~~~V~~~~D~~~~K~~~~Q~~~~C~~~~Q~~~~I~~~~N~~~~T~~~~D~~~~N~~~~E~~~~K~~~~L~~~~S~~~~N~~~~V~~~~Y~~~~L~~~~T~~~~V~~~~D~~~~-G~~~~T~~~~S~~~~K~~~~V~~~~R~~~~-D~~~~D~~~~G~~~~K~~~~Y~~~~F~~~~D~~~~G~~ 589

Db 2315 G--LWNFREKEG-----DCKGCTVSPQVEDSEGTIQFDG 2346

RESULT 15 US-08-125-077-4

Sequence 4, Application US/08125077

Patent No. 587231

Patent No. 587231 5840863

GENERAL INFORMATION:

APPLICANT: Engvall, Eva

APPLICANT: Leivo, Ilmo

TITLE OF INVENTION: Nucleic Acids Encoding Merosin, Merosin

TITLE OF INVENTION: Fragments and Uses Thereof

NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Campbell and Flores
 STREET: 4370 La Jolla Village Drive, Suite 700
 CITY: San Diego
 STATE: California
 COUNTRY: USA
 ZIP: 92122

COMPUTER READABLE FORM:
 COMPUTER TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/125,077
 FILING DATE: 22-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/919,951
 FILING DATE: 27-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Kathryn A.
 REGISTRATION NUMBER: 31,815
 PRIORITY NUMBER: P-LA 9721
 REFERENCE/DOCKET NUMBER: P-LA 9721
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3111 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-125-077-4

Query Match 6.0% Score 186.5: DB 2; Length 3111;
 Best Local Similarity 19.9%; Pred. No. 0.013; Gaps 32;
 Matches 142; Conservative 102; Mismatches 256; Indels 215; Gaps 32;

QY 28 NNQI~~K~~KEET----NN~~D~~~~G~~~~I~~~~E~~~~K~~~~R~~~~S~~~~D~~~~R~~~~T~~~~E~~~~S~~~~T~~~~N~~~~D~~~~E~~~~A~~~~T~~~~F~~~~L~~~~Q~~~~K~~~~T~~~~F~~~~D~~~~N~~~~H~~~~T~~~~I~~~~E~~ 78
 Db 1694 NEKA~~I~~~~N~~~~E~~~~T~~~~G~~~~R~~~~D~~~~E~~~~F~~~~R~~~~N~~~~E~~~~G~~~~L~~~~Q~~~~K~~~~-----EIDOMIKELRKRNLETOKAED 1743~~

QY 79 EYK~~S~~~~V~~~~E~~~~S~~~~S~~~~N~~~~S~~~~I~~~~D~~~~T~~~~A~~~~Q~~~~P~~~~S~~~~H~~~~T~~~~T~~~~I~~~~---~~~~R~~~~E~~~~E~~~~S~~~~V~~~~O~~~~T~~~~S~~~~D~~~~N~~~~E~~~~D~~~~-HVSDFANSKIRESN- 133~~

1744 ELVAEA~~L~~~~K~~~~V~~~~K~~~~L~~~~G~~~~E~~~~S~~~~R~~~~G~~~~E~~~~N~~~~E~~~~M~~~~K~~~~D~~~~R~~~~E~~~~K~~~~Y~~~~N~~~~V~~~~D~~~~A~~~~W~~~~D~~~~L~~~~R~~~~E~~~~A~~~~T~~~~D~~~~K~~~~I~~~~R~~~~A~~~~N~~~~R~~ 1803

QY 134 -----TESKE--ENTIOPNKV-----KEDSTS 156
 1804 LFAVNOKNM~~T~~~~A~~~~L~~~~K~~~~K~~~~E~~~~A~~~~V~~~~E~~~~S~~~~G~~~~K~~~~R~~~~Q~~~~E~~~~N~~~~T~~~~L~~~~K~~~~E~~~~G~~~~N~~~~D~~~~I~~~~L~~~~R~~~~T~~~~Y~~~~D~~~~I~~~~Q~~~~T~~~~K~~~~1~~ 1863

QY 157 QPSGYTN~~I~~~~E~~~~K~~~~I~~~~S~~~~N~~~~-----QDELLNLPINEENKARPLISTSA---QPSIKRVVNQL 206~~

Db 1864 LPMSE~~E~~~~N~~~~D~~~~K~~~~D~~~~L~~~~S~~~~Q~~~~E~~~~I~~~~K~~~~L~~~~A~~~~E~~~~V~~~~S~~~~Q~~~~A~~~~E~~~~H~~~~Q~~~~A~~~~N~~~~D~~~~S~~~~A~~~~V~~~~L~~~~G~~~~I~~~~D~~~~K~~~~-----SFRNAT 1923~~

QY 207 AAEQG-SVNVHLIKVTDOSITEGYDSEGVIKAHDENLYIVTIEVDVKYRGDTMTVD 265

Db 1924 AAFKAYSN~~I~~~~K~~~~Y~~~~-----DRAEKVAK--EAKDLAHEAT----KLATGPR--G 1962~~

QY 266 IDKNTVPSLTSFTI-----PKNDNSEIATGT----YDNKNQI~~T~~~~Y~~~~F~~~~D~~~~Y~~~~V~~~~D~~~~3~~ 313

Db 1963 LKKEDAKGCLOSKSFRILNEAKKLANDKVENDEDHNGLKTRIENALARNGDARNGDILRTNLDTLG 2022

QY 314 KYENI--KAHLKLTSYIDSKVPPNNTK-----LDEYKTA~~L~~~~S~~~~V~~~~N~~~~K~~~~T~~~~I~~~~T~~~~3~~ 356

Db 2023 KLSAIPND~~T~~~~A~~~~K~~~~Q~~~~D~~~~K~~~~A~~~~R~~~~Q~~~~Q~~~~-----LDAQTELHONLDGLKKYKLADSAVKTNA 2082~~

QY 357 VEVORPNENR-TANLQSMFTNID-----TKNUTVEOTYINPLRY 396
Dp | ; | : | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
Dp 2083 V-VKDSKNKTTADADATVKNEQERADRLIDKLPKELEDNLKKNISEIKELINQARKO 2141
QY 397 ABEVNWNISGND-----EGS-----TIIDSTTIKV-----YK 425
Dp | ; | : | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
Dp 2142 ANSIKVSSGGDCIRYKPEKKGSNNIVNVKTAVADNLFLYLGSAKIDFLAEMR 2201
QY 426 VCDNQNLPPSNRIVDSEYEVNTDD-----YADIGNNNDVNINEGNIDSPYIKVIS 478
Dp | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
Dp 2202 KCKVSFLMDVGSGVGRVEYPDLTIDDSWYWRIVASRTGRNSTISVR--ALDGPKASIVPS 2259
QY 479 -KYBPKHDDYTIIQQTVMOITINETGEFRASINTIASSTSSQGQGLPPTYKI 537
Dp | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
Dp 2260 THHSTSPGVTILDVANAMIFVGGUTGKLUKKADAVRVITFGCMGETYFINKP---I 2314
QY 538 GYVWEDVDKDQTNTNEKPLSINVLTATPD-GTSKSVRT-DEDGKYQFDG 589
Dp | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; | ; |
Dp 2315 G-LWNFREKES-----DCRQCTIVSFQVEDSEGTTIQFDG 2346

Search completed: July 30, 2002, 10:32:10
Job time: 195 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 30, 2002, 10:28:55 ; Search time 52.53 Seconds
(without alignments)
1084.732 Million cell updates/sec

Title: US-09-147-405-11
Sequence: 1 HHHHHKPSSDDEKNDVNNN.....SKSVRPTDEDGYQFPGVQVD 593
Scoring table: BLOSUM62
GapPen 10.0 , Gapext 0.5

searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR71:
1: Pirl:
2: Pir2:
3: Pir3:
4: Pir4:
5: Pir5:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Length	DB ID	Description	
1	3015	97.7	1092	2 T30214	fibrinogen-binding protein - <i>Staphylococcus epidermidis</i>
2	146.5	37.1	1166	2 T30214	C.Species: <i>Staphylococcus epidermidis</i>
3	1139.5	36.9	1141	2 E89824	C.Date: 22-oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-May-2000
4	576	18.7	1315	2 T28680	C.Accession: T30214
5	559	18.1	1385	2 D8824	R.Nilsson, M.; Frykberg, L.; Flock, J.I.; Pei, L.; Lindberg, M.; Guss, B.
6	490	15.9	953	2 C89824	Infect. Immun. 66, 2665-2673, 1998
7	452	14.6	933	2 S41539	A.Title: A Fibrinogen binding protein of <i>Staphylococcus epidermidis</i> .
8	452	14.6	989	2 D89825	A.Reference number: Z20781; MUID:9826511
9	405.5	13.1	877	2 F90070	A:Accession: T30214
10	376	12.2	940	2 S19702	A.Status: preliminary; translated from GB/EMBL/DDJB
11	345.5	11.2	961	2 G90053	A.Molecule type: DNA
12	326	10.6	1038	2 H90053	A:Cross-references: EMBL:Y17116; NID:e1296734; PID:e1296735; PIDN:CAA76638.1
13	304	9.8	1018	2 A32192	RESULT 1
14	239	7.7	1039	2 T30856	Query Match 97.7%; Score 3015; DB 2; Length 1092;
15	225	7.3	1463	2 T30290	Best Local Similarity 99.7%; Pred. No. 9.6-12%; Mismatches 0; Indels 0; Gaps 0
16	222	7.2	1711	2 T18429	Db 75 SSDEEKNDVNNNQSINTDDNNQTIKKETTNNDGIEKRSEDDETESTNWDENATEFLQK 67
17	221.5	7.2	1959	2 AGI085	Oy fibrinogen-binding protein - <i>Staphylococcus epidermidis</i>
18	216.5	7.0	3394	2 T18501	Db 75 SSDEEKNDVNNNQSINTDDNNQTIKKETTNNDGIEKRSEDDETESTNWDENATEFLQK 134
19	214	6.9	1093	2 T18275	Oy fibrinogen-binding protein - <i>Staphylococcus epidermidis</i>
20	213.5	6.9	2206	2 G71611	Db 68 TPODNTHLETEEEKESSYESSNSIDTAQPSHTTNEESWQTSDNVEDSAVSDFANS 127
21	213	6.9	821	2 S67087	Oy KIKESNTESGKEEENTIEQPNVKVEDSTTSQPSGYNIDENKISNODELNLNLPINEYENKAR 254
22	212.5	6.9	1125	2 E90598	Db 135 TPODNTHLETEEEKESSYESSNSIDTAQPSHTTNEESWQTSDNVEDSAVSDFANS 194
23	211.5	6.9	3774	2 T18427	Oy 128 KIKESNTESGKEEENTIEQPNVKVEDSTTSQPSGYNIDENKISNODELNLNLPINEYENKAR 187
24	209	6.8	4550	2 T18440	Db 195 KIKESNTESGKEEENTIEQPNVKVEDSTTSQPSGYNIDENKISNODELNLNLPINEYENKAR 247
25	208.5	6.8	1072	2 A86227	Oy 255 PLSPSTSQAQPSIKRVYNOQAAEDGSNVNLKIVDOSTEGYDSEGVKAHDENLYD 314
26	208	6.7	1127	2 T28517	Db 308 FTDVVKYENIKAHKLTSYIDSKSPVNNTKLQVEYKPAASSVKTINVEYORPNEQT 367
27	207.5	6.7	2401	2 T28576	Oy 315 VTFEVDDKWKSGDTMTVDIDKNTVFSDLTSDFITFKIKONSGEIAITGYDNKNQIYT 374
28	207	6.7	769	2 F89870	Db 324 ANIQSMFTNDKHNHIVTEOTIYINPLRSAKERWNWNSONGDGEOSTIIDSTIKVKG 427
29	207	6.7	1939	2 T18372	Oy 368 ANIQSMFTNDKHNHIVTEOTIYINPLRSAKERWNWNSONGDGEOSTIIDSTIKVKG 494

alignments

surface-located m

Im1 protein - Myc
hypothetical protein
fimB protein [impoo
asparagine/sparia
asparagine-rich PR
DNA helicase II PR
ribophry protein -
probable membrane
hypothetical prote
hypothetical prote
hypothetical prote
sensory transducti
cytadherence-acces
hypothetical prote
similar to late em

OY	488	TQIQTQVMTQTTINETYGEFRASYNTAFTSSGOGQDIPPEKTYKIGQYWEDVK	547	Db	555	TIQQTQVMTQTTINETYGEFRASYNTAFTSSGOGQDIPPEKTYKIGQYWEDVK	614				
OY	540	DGTONNEKEPIISNVYLTIPDGTSYSVRUDGKQFQDVQ	591	Db	615	DGTONNEKEPIISNVYLTIPDGTSYSVRUDGKQFQDVQ	658				
RESULT	2	fibrinogen-binding protein homolog - <i>Staphylococcus aureus</i>		RESULT	3	hypothetical protein_sdre [imported] - <i>Staphylococcus aureus</i> (strain N315)					
Query	T28680	C.Species: <i>Staphylococcus aureus</i>		Query	EB9824	C.Species: <i>Staphylococcus aureus</i>					
OY	8	C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000		Db	646	C.Accession: E89824					
Db	66	C;Accession: T28680		Db	647	R.Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizutani-Uti, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.					
OY	66	C;Accession: T28680		Db	648	A.TITLE: Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> .					
Db	66	C;Accession: T28680		Db	649	A;Reference number: A89758; MUID:21311952; PMID:11418146					
OY	66	A;Status: preliminary		Db	650	A;Accession: E89824					
Db	124	A;Cross-references: T28680		Db	651	A;Status: preliminary					
OY	123	A;Molecule type: DNA		Db	652	A;Molecule type: DNA					
Db	173	A;Cross-references: EMBL:AD005647; NID:e1318793; PID:e1318794; PIDN:CAAG6652.1		Db	653	A;Residues: 1-1141 <JOB>					
OY	179	A;Cross-references: EMBL:AD005647; NID:e1318793; PID:e1318794; PIDN:CAAG6652.1		Db	654	A;Experimental source: strain N315					
OY	230	A;Genetics: sdre		Db	655	A;Genetics: sdre					
Query	Match	37.1%	Score 1146.5;	DB 2;	Length 1166;	Query	Match	36.9%	Score 1139.5;	DB 2;	Length 1141;
Best	Local	Similarity	Pred. No.	Mismatches	Indels	Best	Local	Similarity	Pred. No.	Mismatches	Indels
Matches	263;	Conservative	8.4e-42;	191;	Gaps	Matches	266;	Conservative	1.6e-41;	193;	Gaps
OY	8	SDEEKNDVINVNNQSINTDDNOI--IKKEENNDDNIKEKRERDTSTINDENEATFLQ	67	Db	69	SDKEEVVSETENNSTENDSINPI--KRENT--DSOPEAKEESTTSSQQONNVATE	125	Db	69	SDKEEVVSETENNSTENDSINPI--KRENT--DSOPEAKEESTTSSQQONNVATE	125
Db	66	ATVDNKENVSETENNSTENDSINPI--TNTDOSPEAKESTTSSQQONNVATE	123	Db	68	TPODNTHITTEEVKES--SSVESSNSSSIDAQPSHTTNREESVOTSNDVEDSHVS	122	Db	70	TPODNTHITTEEVKES--SSVESSNSSSIDAQPSHTTNREESVOTSNDVEDSHVS	124
OY	66	QKTPQDNTHLTEREVKES--SSVESSNSSSIDAQPSHTTNREESVOTSNDVEDSHVS	122	Db	126	TKPON--TEKENVKPSTDKTATEDTSVILEEKAPNT--NNDVDTPKS-----TS	172	Db	126	TKPON--TEKENVKPSTDKTATEDTSVILEEKAPNT--NNDVDTPKS-----TS	172
Db	124	TEKPON--TEKENVKPSTDKTATEDTSVILEEKAPNT--NNDVDTPKS-----TS	172	Db	125	ANSKIKESNT--ESEGKENTIEQPNKVKEDSTSOPSGYNTIDEKIS-NODELLNP--	178	Db	125	ANSKIKESNT--ESEGKENTIEQPNKVKEDSTSOPSGYNTIDEKIS-NODELLNP--	178
OY	123	DFANSKIKESEN--ESEGKENTIEQPNKVKEDSTSOPSGYNTIDEKIS-NODELLNP	178	Db	171	-TSEIQPKTPOESTNENSOQPOTPSKV--NNQVTDATNPKEPVNNVSKELKNPEK	226	Db	171	-TSEIQPKTPOESTNENSOQPOTPSKV--NNQVTDATNPKEPVNNVSKELKNPEK	226
Db	173	EPSTSEIOTKPTPOESTNENSOQPOTPSKV--NNQVTDATNPKEPVNNVSKELKNPEK	229	Db	179	-----INEYENKARPLSTSAQNSIKR-----TWNQLAEGOSNNVNLIKVTDQ	223	Db	179	-----INEYENKARPLSTSAQNSIKR-----TWNQLAEGOSNNVNLIKVTDQ	225
OY	179	-----INEYENKARPLSTSAQNSIKR-----TWNQLAEGOSNNVNLIKVTDQ	223	Db	227	LKLVRNNNDNIDRSTKFVATPAPTSVAKPLNAKMRFAWQPARAVASNNVNNDLITVQKTI	286	Db	227	LKLVRNNNDNIDRSTKFVATPAPTSVAKPLNAKMRFAWQPARAVASNNVNNDLITVQKTI	286
OY	220	EKIKELVRNNDNIDRSTKFVATPAPTSVAKPLNAKMRFAWQPARAVASNNVNNDLITVQKTI	289	Db	226	TSGYDDEGGVIAHDANLIVYTFEUDKVSQDTMVTDKNTVPSLDTSFTPK	285	Db	226	TSGYDDEGGVIAHDANLIVYTFEUDKVSQDTMVTDKNTVPSLDTSFTPK	285
Db	290	STEGYDDEGGVIAHDANLIVYTFEUDKVSQDTMVTDKNTVPSLDTSFTPK	283	Db	287	KVG-DGKDNVAAHGDGKDIYEDEFTTDINKVKQGDTMINTDKNVNIPSLDTKDNPIDT	345	Db	287	KVG-DGKDNVAAHGDGKDIYEDEFTTDINKVKQGDTMINTDKNVNIPSLDTKDNPIDT	345
OY	284	TIKVG-DGKDNVAAHGDGKDIYEDEFTTDINKVKQGDTMINTDKNVNIPSLDTKDNPID	348	Db	288	DNGEITATGTYDNNKQKQITYFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	345	Db	288	DNGEITATGTYDNNKQKQITYFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	345
Db	349	TKNGNGETIATGTYDNNKQKQITYFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	343	Db	346	TKNGNGETIATGTYDNNKQKQITYFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	404	Db	346	TKNGNGETIATGTYDNNKQKQITYFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	404
OY	344	349 IDPSGEVIAKGFGDKATQIYTFTDVKYENKIAHKLTSYIDSKVPPNNTKLOVEK	407	Db	405	TALSVNKTIVTYQRPNENRTANLQSMFNIDTNTKHNTVQTYTIPLYSAKETNNIS	405	Db	405	TALSVNKTIVTYQRPNENRTANLQSMFNIDTNTKHNTVQTYTIPLYSAKETNNIS	405
Db	408	YKPALOSSNKTIVTYQRPNENRTANLQSMFNIDTNTKHNTVQTYTIPLYSAKETNNIS	403	Db	406	TAGKTESONVSYDQPMVHGDSNQSFIFTKLDENKOTIEQQIVYPLKKTATNKVDA	464	Db	406	TAGKTESONVSYDQPMVHGDSNQSFIFTKLDENKOTIEQQIVYPLKKTATNKVDA	464
OY	404	FATAGKTESONVSYDQPMVHGDSNQSFIFTKLDENKOTIEQQIVYPLKKTATNKVDA	467	Db	407	GNG-----DEGSTIDDSTIKVYKGUNQNLDSNRVYDSEYDVTND-YQAL	455	Db	407	GNG-----DEGSTIDDSTIKVYKGUNQNLDSNRVYDSEYDVTND-YQAL	455
Db	528	ISGNG-----DEGSTIDDSTIKVYKGUNQNLDSNRVYDSEYDVTND-YQAL	453	Db	465	GSQVDDYGNKLGNGSTIDQNTKLEIKVKNQNLQPSNRLYDFSOEDNPKS	524	Db	465	GSQVDDYGNKLGNGSTIDQNTKLEIKVKNQNLQPSNRLYDFSOEDNPKS	524
Db	468	IAGSQVDDYGNKLGNGSTIDQNTKLEIKVKNQNLQPSNRLYDFSOEDNPKS	527	Db	456	GINNDVINFQGNDSPYIPIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	515	Db	456	GINNDVINFQGNDSPYIPIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	515
OY	454	QLGNNNDVINFQGNDSPYIPIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	513	Db	525	FENNTIDDFGDSINSATXIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	582	Db	525	FENNTIDDFGDSINSATXIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	582
Db	528	KSTFSNNVATQDGDINSAYIKVSKYDNDKDYTTQTYTQTTINETYGEFRASYNT	585	Db	516	IAPSTSGQGQDLPPEKTYKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	574	Db	516	IAPSTSGQGQDLPPEKTYKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	574
OY	514	NTIAFSTSSGQGQDLPPEKTYKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	572	Db	583	IVTSNDPQGGDTVPEEKJJKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	642	Db	583	IVTSNDPQGGDTVPEEKJJKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	642
Db	566	NEVITSNDPQGGDTVPEEKJJKIGQYWEDVKDGTQONTNEKEPLSNVLTVYDGT	645	Db	575	KSVTDEDKYQFDGVQ	591	Db	575	KSVTDEDKYQFDGVQ	591

Db	643 KSVRTDANGHYEFGGLK 659	hypothetical protein <i>sdrd</i> [imported] - <i>Staphylococcus aureus</i> (strain N315)
RESULT	4	C;Species: <i>Staphylococcus aureus</i>
T28679	fibrinogen-binding protein homolog - <i>Staphylococcus aureus</i>	C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Species: <i>Staphylococcus aureus</i>	C;Accession: D89824	R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K;Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-May-2000	A;Title: Whole genome sequencing of meticillin-resistant <i>Staphylococcus aureus</i> .	Lancet 357, 1225-1240, 2001
C;Accession: T28679	A;Reference number: A89758; MUID:21311952; PMID:11418146	A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Status: preliminary	A;Accession: D89824	A;Accession: D89824
A;Molecule type: DNA	A;Status: preliminary	A;Status: preliminary
A;Cross-references: EMBL:AJ005646; NID:e1318791; PID:e1318792; PIDN:CAA06651.1	A;Cross-references: GB:PA000018; PID:913700454; PIDN:BA841751.1; GSPDB:GN00149	A;Experimental source: strain N315
C;Genetics:	C;Genetics:	C;Genetics:
A;Gene: sdrd	A;Gene: sdrd	A;Gene: sdrd
Query Match 18.7%; Score 576; DB 2; Length 1315;	Query Match 18.1%; Score 559; DB 2; Length 1385;	Query Match 18.1%; Score 559; DB 2; Length 1385;
Best Local Similarity 30.1%; Pred. No. 2.4e-17;	Best Local Similarity 28.8%; Pred. No. 1.4e-16;	Best Local Similarity 28.8%; Pred. No. 1.4e-16;
Matches 185; Conservative 112; Mismatches 228; Indels 92; Gaps 29;	Matches 177; Conservative 117; Mismatches 235; Indels 86; Gaps 27;	Matches 177; Conservative 117; Mismatches 235; Indels 86; Gaps 27;
QY 8 SSDERKNDV--INNOQSINTDDNNQIIRKEETNNYDGTEKRSDRTESTTNVDE-NEAT 63	QY 8 SSDERKNDV--INNOQSINTDDNNQIIRKEETNNYDGTEKRSDRTESTTNVDE-NEAT 63	QY 8 SSDERKNDV--INNOQSINTDDNNQIIRKEETNNYDGTEKRSDRTESTTNVDE-NEAT 63
Db 55 STNKELNEATTSASDNQSSDKVDQQLNEDNTNDKRNQEMVSQNETTSNGKLIKE 114	Db 55 STNKELNEATTSASDNQSSDKVDQQLNEDNTNDKRNQEMVSQNETTSNGKLIKE 114	Db 55 STNKELNEATTSASDNQSSDKVDQQLNEDNTNDKRNQEMVSQNETTSNGKLIKE 114
QY 64 FLOQIPQDQWHLTBEEVKPSSVSVSSNSSTDQAPSHTTINRERSVOSDNDVSHVD 123	QY 64 FLOQIPQDQWHLTBEEVKPSSVSVSSNSSTDQAPSHTTINRERSVOSDNDVSHVD 123	QY 64 FLOQIPQDQWHLTBEEVKPSSVSVSSNSSTDQAPSHTTINRERSVOSDNDVSHVD 123
Db 115 SVQSTGNGKVEVSTAKSDEQASPKSTNDLTKO---TISNOBALQ-PDLQENKSVN 168	Db 115 SVQSTGNGKVEVSTAKSDEQASPKSTNDLTKO---TISNOBALQ-PDLQENKSVN 168	Db 115 SVQSTGNGKVEVSTAKSDEQASPKSTNDLTKO---TISNOBALQ-PDLQENKSVN 168
QY 124 FANSKIKESTESGEKEENTEQPKNVKESTDTSQPSGYNI-DEKISNDELL-NLPIN 180	QY 124 FANSKIKESTESGEKEENTEQPKNVKESTDTSQPSGYNI-DEKISNDELL-NLPIN 180	QY 124 FANSKIKESTESGEKEENTEQPKNVKESTDTSQPSGYNI-DEKISNDELL-NLPIN 180
Db 169 ---VOPTHEEENKVKD-----AKTEST-----LAVKSKAIAKSNDETLVDDNSNS 209	Db 169 ---VOPTHEEENKVKD-----AKTEST-----LAVKSKAIAKSNDETLVDDNSNS 209	Db 169 ---VOPTHEEENKVKD-----AKTEST-----LAVKSKAIAKSNDETLVDDNSNS 209
QY 181 EYENKARPLSTTSQAP---SIKRVTVNOLAAEGSNNVNLILKTYDOSITEGYDSEGVI 236	QY 181 EYENKARPLSTTSQAP---SIKRVTVNOLAAEGSNNVNLILKTYDOSITEGYDSEGVI 236	QY 181 EYENKARPLSTTSQAP---SIKRVTVNOLAAEGSNNVNLILKTYDOSITEGYDSEGVI 236
Db 210 NNEENNADILRKSTARKEMLRMRAVQPSSTEAKRNVLNLTISNLTIVDVKNNKV 269	Db 210 NNEENNADILRKSTARKEMLRMRAVQPSSTEAKRNVLNLTISNLTIVDVKNNKV 269	Db 210 NNEENNADILRKSTARKEMLRMRAVQPSSTEAKRNVLNLTISNLTIVDVKNNKV 269
QY 237 KAHDENLIYDVFTEVDKVKSGDTMTIDKNTV-----PSDLATDFMPKRD-NSG 289	QY 237 KAHDENLIYDVFTEVDKVKSGDTMTIDKNTV-----PSDLATDFMPKRD-NSG 289	QY 237 KAHDENLIYDVFTEVDKVKSGDTMTIDKNTV-----PSDLATDFMPKRD-NSG 289
Db 270 PQAQYLSLKSQT---VDDKVKGDFITK-SDTVQVYGLNPEDIKN--IGDIDKPNNG 323	Db 270 PQAQYLSLKSQT---VDDKVKGDFITK-SDTVQVYGLNPEDIKN--IGDIDKPNNG 323	Db 270 PQAQYLSLKSQT---VDDKVKGDFITK-SDTVQVYGLNPEDIKN--IGDIDKPNNG 323
QY 290 EIIATCYYDVKNKQIITYDVYDVKENIAHKLTSYIJKSKVPINNTKDVEKTALS 349	QY 290 EIIATCYYDVKNKQIITYDVYDVKENIAHKLTSYIJKSKVPINNTKDVEKTALS 349	QY 290 EIIATCYYDVKNKQIITYDVYDVKENIAHKLTSYIJKSKVPINNTKDVEKTALS 349
Db 324 ETIAKAKHDPTANLLITYTFDYDVFRENSVONGINYNTYMDATIP--VSKNDVFRNTIG 381	Db 324 ETIAKAKHDPTANLLITYTFDYDVFRENSVONGINYNTYMDATIP--VSKNDVFRNTIG 381	Db 324 ETIAKAKHDPTANLLITYTFDYDVFRENSVONGINYNTYMDATIP--VSKNDVFRNTIG 381
QY 350 SVNKTITVEYKORP--ENRTANLQSMFTNIDTKNT-----VEQTIYINPLRYSAKE 399	QY 350 SVNKTITVEYKORP--ENRTANLQSMFTNIDTKNT-----VEQTIYINPLRYSAKE 399	QY 350 SVNKTITVEYKORP--ENRTANLQSMFTNIDTKNT-----VEQTIYINPLRYSAKE 399
Db 382 NTTTKTANTAOYDPYVNEKSAFT--EVYVHGNKENPGYQYIYVNPNSLTN 439	Db 382 NTTTKTANTAOYDPYVNEKSAFT--EVYVHGNKENPGYQYIYVNPNSLTN 439	Db 382 NTTTKTANTAOYDPYVNEKSAFT--EVYVHGNKENPGYQYIYVNPNSLTN 439
QY 400 TNNTI---SENGDEGSTIIDDSTIIRKVYGVGDQNULPDSNRIVY'S--EVEDVTNDYA 453	QY 400 TNNTI---SENGDEGSTIIDDSTIIRKVYGVGDQNULPDSNRIVY'S--EVEDVTNDYA 453	QY 400 TNNTI---SENGDEGSTIIDDSTIIRKVYGVGDQNULPDSNRIVY'S--EVEDVTNDYA 453
Db 440 AKLKVGAYHSSPPNNIQINKVTDIKIQVPKGYIL--NKGYDWNTKETDVN-QYL 495	Db 440 AKLKVGAYHSSPPNNIQINKVTDIKIQVPKGYIL--NKGYDWNTKETDVN-QYL 495	Db 440 AKLKVGAYHSSPPNNIQINKVTDIKIQVPKGYIL--NKGYDWNTKETDVN-QYL 495
QY 454 Q---LGNNNDNINFGNMDSPVPIKIVSKVPPNKKDYTITQOTVHOTTINETYGRFTA 510	QY 454 Q---LGNNNDNINFGNMDSPVPIKIVSKVPPNKKDYTITQOTVHOTTINETYGRFTA 510	QY 454 Q---LGNNNDNINFGNMDSPVPIKIVSKVPPNKKDYTITQOTVHOTTINETYGRFTA 510
Db 496 QKITYGDNSAVTDFGNADSAVVMNTKFOVTNSESPTLVOMATLSSTGN----KSV 549	Db 496 QKITYGDNSAVTDFGNADSAVVMNTKFOVTNSESPTLVOMATLSSTGN----KSV 549	Db 496 QKITYGDNSAVTDFGNADSAVVMNTKFOVTNSESPTLVOMATLSSTGN----KSV 549
QY 511 SYDNTAFASTISSGGQGDLPBPBKTYKGDVWDVKDQGIONTNDNEKPLSNVLMVLYT 570	QY 511 SYDNTAFASTISSGGQGDLPBPBKTYKGDVWDVKDQGIONTNDNEKPLSNVLMVLYT 570	QY 511 SYDNTAFASTISSGGQGDLPBPBKTYKGDVWDVKDQGIONTNDNEKPLSNVLMVLYT 570
Db 550 STGAGNAGFTNINQGGAG---QEVYKIGNYVWEDTNKGVOIL--GEKGVGNVTV-FDN 602	Db 550 STGAGNAGFTNINQGGAG---QEVYKIGNYVWEDTNKGVOIL--GEKGVGNVTV-FDN 602	Db 550 STGAGNAGFTNINQGGAG---QEVYKIGNYVWEDTNKGVOIL--GEKGVGNVTV-FDN 602
QY 571 DGTTSKSR--TDEDGKY 585	QY 571 DGTTSKSR--TDEDGKY 585	QY 571 DGTTSKSR--TDEDGKY 585
Db 603 NNNTTKVGEAVTKEDGSY 620	Db 603 NNNTTKVGEAVTKEDGSY 620	Db 603 NNNTTKVGEAVTKEDGSY 620
RESULT 6	RESULT 6	RESULT 6
Db 9824	hypothetical protein <i>sdrd</i> [imported] - <i>Staphylococcus aureus</i> (strain N315)	hypothetical protein <i>sdrd</i> [imported] - <i>Staphylococcus aureus</i> (strain N315)
C;Species: <i>Staphylococcus aureus</i>	C;Species: <i>Staphylococcus aureus</i>	C;Species: <i>Staphylococcus aureus</i>

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: C09824
 C;Status: preliminary
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguri, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Cma, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: C09824
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:BA000018; PID:g13700453; PIDN:BAB41750.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: sdrC

Query Match 15.9%; Score 490; DB 2; Length 953;
 Best Local Similarity 28.2%; Pred. No. 7.7e-4;
 Matches 162; Conservative 83; Mismatches 236; Indels 94; Gaps 22;

QY 42 GIEKRSEDRTESTINVDENEATFLQKTPQDWTILTHEEKKESSVSESSNSSIDTAQPSH 101
 DB 45 GHEAKAEGHTNGELNGSKNETT---APSEN--TTEKV--DSRQLKDNTQATADPKV 96
 QY 102 TTINREESVQISDNVEDSHVSDFANSKIKESENTEQPNVKVEDSITSGY 161
 DB 97 T-----MSDASATKETSSNMQS-----PONATASQSTQTSNV 129
 QY 162 TNIDEK--ISNQDELLNLPINEYEN-KARPLSTSRAOPSIRKRVTVNOLAA-EQGSNVNH 216
 DB 130 TNDKSSTTYSNEDTKDSL--TQAKNVSTTPKTTIKORALNRMAVTVAAPQQGIVND 187
 QY 217 LIKVTDOSI-----TEGDSECVIAKAHDENIYDVFEVDKVKSDMT 263
 DB 188 KVHFPTNDIAIBKGHVNTTGNTWETATSSDVLY-----LXANTITDDSVKEGDT 239
 QY 264 VDIDKNTVPSIDJDSFTIPKIKDNGNSEGIATQTYDNKNQQTTFDIDVYENIKAHKLH 323
 DB 240 FKYQGVFRPGSLRPLSPTQTONLNAQGNTIAKGDSKTNTTYYTFTDYNVGSFEE 299
 QY 324 LTSYDIDSKVPPNNTKLDEVYKHALSVNKTTVEYCORPNEARTNQSMFTNDKHNTH 383
 DB 300 QVAFAKRENATDKTAKMENVTLGNDTYSKDWIVDY--GNQKGQOLISSTWYINNEDLS 356
 ~~~ 384 VECTIYIN-PLRS-AKEVN-NISGNGDEGSTTIDSTTIKYKVGUNONLFDNSRHYD 441  
 357 RNMVYVNPQPKTYKTYTFTVNLN-----GYKFNPDAKNEFKYEVTDONQFDS-FTPDT 410  
 QY 442 SEFDVTDND-DYQALGNNDNINVNGN---IDSPYIIVKVIKDPNKKDVTIQQVTM 496  
 DB 411 SKIUDVQGDFDVIYISNDNKTAVDLDINGQSSDQKQYIIQVAVPDNSTDNCRKYDYLET 470  
 QY 497 QTTINEYTGEGERTASYDNTIAFSTSSGGQGQDLPPEKTYKIGDIWEDVDKQGINTND 556  
 DB 471 QNGKSSWSN----SYSNVNGSSTANGI-----QKVNGLGDYIWEDTNKGQKDA--N 516  
 QY 557 EKPLSNUVLUTLTYPDGTS-KSVRDEDKYQFQGV 590  
 DB 517 EKGIGKGVVYLKDNGKELDRTTIDENGKYQFTGL 551  
 RESULT 7  
 S41539 fibrinogen-binding protein - *Staphylococcus aureus*  
 N;Alternate names: clumping factor  
 C;Species: *Staphylococcus aureus*  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 15-Oct-1999  
 C;Accession: S41539; S3630  
 R;Medevitt, D.; Francois, P.; vaudaux, P.; Foster, T. J.  
 Mol Microbiol 11, 27-248, 1994  
 A;Title: Molecular characterization of the clumping factor (fibrinogen receptor) of Staph

A;Reference number: S41539; MUID:94224142  
 A;Accession: S41539  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-933 <KUR>  
 A;Cross-references: GB:BA000018; PID:g13700678; PIDN:BAB41975.1; GSPDB:GN00149  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: clfa

Query Match 14.6%; Score 452; DB 2; Length 933;  
 Best Local Similarity 26.6%; Pred. No. 3.1e-12;  
 Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;

QY 8 SSDEEKNDVNNQSIINTDDNNQIIRKETNNYDGIEKRSBDRTESTNTDENERATFLQK 67  
 DB 51 SNEKSNDSSSYSAAPKTTDNV-----SDTKTSNTN--NGTSVAQ 91  
 QY 68 TPQDNWHLTEEVKSSSVSSNSNSIDTAQPSHTTINREBSVQFSDNTVSDSHVSDFANS 127  
 DB 92 NP-----AQETTQSSTNATTEETPTVIGATTNTQANTPATQS-SNTNAELVN- 143  
 QY 128 KIKESTSSEGKREENTIEQPNVKVEDSITSPQSGYINIDEKIISNOBLIN-LPINEVENKA 186  
 DB 144 -QTSNETTENDNTV-----SSVNSPONSTNAENYSTQDTS-TATPSN--NES 189  
 QY 187 RPLSTMSAQPSKTRVTVN-----QLAEQGSVNHNLIKVTD--SITEGYDSEGV 235  
 DB 190 APQSTDASHKDVQVNAQNTSPRMRAESLAVAADPAGDITNOLNTVNGI-DSGT 248  
 QY 236 IKAHDENIYDVFEVDKVKSDMT 295  
 DB 249 VPHQHOGYVKLNQGFSVPSAVKGDFFKTVPEKLNLGVISTAKVFFIMGD-QVLAN 307  
 QY 296 TYDNNKQIQTFTDQDVYKENIKAHLTYSIDKSKVNPNTKL-DVEYKTAASS--VN 352  
 DB 308 VIDS-DGCVVIFTDYNVTKDVKATLMPAVD---PEVVKGTGNTVLAIGSTAN 362  
 QY 353 KTIVEXQRPNERNTANLQSMFTNDTNNKHTVEQTYINPL--RYSAKETVNISONGE 410  
 DB 363 KVLVLDYKEKGKFYNLSKIGTIDQDQKNTPTROTVINPSPGDNVTAFLVQGLNPNTD 422  
 QY 411 GSTTIDDDSTTIKYKVGUNONLFDNSRHYDSEYDVNDYAQLGNNNDVNING--- 466  
 DB 423 NALDOONNTISKVYKVDNADISESYV--NPENFEDTINSVITFPNNQKVENPDD 481  
 QY 467 NDSPYIIVKVIKYDPNKKDVTIQQVTMOTNTINETGE--FRTASYDNTIAFSTSSG 523  
 DB 482 QTWTPYTVVNGHIDPNSKD-----LALRSTLYGINSNIWRSMSWDNEVAFNNGSG 534  
 QY 524 OGOG-DIF--PEKTYKGDY--WWEVDKQD-GIQTNDN 556  
 DB 535 SGDGDIPKVVPDOPDGEIEPIPEDSDSPGSDGSDS 573  
 RESULT 8  
 D09852 fibrinogen-binding protein A, clumping factor [imported] - *Staphylococcus aureus* (str C;Species: *Staphylococcus aureus*  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 C;Accession: D09852  
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Cma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Cma, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.  
 Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A;Reference number: A89758; MUID:21311952; PMID:11418146  
 A;Accession: D09852  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-989 <KUR>  
 A;Cross-references: GB:BA000018; PID:g13700678; PIDN:BAB41975.1; GSPDB:GN00149  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: clfa

Query Match 14.6%; Score 452; DB 2; Length 989;  
 Best Local Similarity 25.9%; Pred. No. 3.4e-12; Mismatches 224; Indels 102; Gaps 27; Matches 152; Conservative 109; N mismatches 224; Indels 102; Gaps 27;

Qy 4 HHHSSEDEENNDVIL--NNNQSINTDDNNQIIKEETNNYDGIERSERTESTSNTNDV 60  
 Db 39 NHQAQASECOENDTQOSSKNNASADESKNNI---ETPOINTTANDTSNTSANTNSAVD 94  

Qy 61 EATFLQTKPODNTLHTEEVKESSSVESSNSSIDTAQQSHTTINREESVQTSNDVWEDSHUSDFANS 120  
 Db 95 STKMKSTQPSNTTTE-----PASTNETPQPTAKNQ--ATAARMODT 137  
 Qy 121 VSDFANSKIKESNTSGKEENTIEOPNKVKEDSTSOPSGYTNTDEKISNODELLNLPIN 180  
 Db 138 VPQEANSQVDNKT--NDANSIATNSELNSQT-----LDLP- 172  
 Qy 187 RPLSTSA-----OPSIKRIVTQNLA-----EGSNNNHLIKVTQDQSITEGID 231  
 Db 173 ---QSPQTISNAQGTSKPSVRARSLAVAEPPVNAADAKGTVN-----DKVTAS 222  
 Qy 190 APontDASNKDVVSQAVNPSTPRMRAFSLAAVADAAPAGDTN--OLTDVKYI--ID 186  
 Db 144 -QTSNETSNTNTV-----SSVNSPONSTNAENVSTDTSTEATPSN--NES 189  
 Qy 232 SEGVIAKAHDENLILYDVFEDDKVKSGDITMV-----DID--KNTVPS 273  
 Db 245 SGTTVYPROAGVWKLNGPSVNPNSAVKGOTKLTIVPKELNLNGTSTARVUPPTMAGD-QV 303  
 Qy 292 IATGYTYDNKNKQTYTFTYDVKYENIKAHKLKLTSYIDKSKVPPNNTKL-DVEKRTAL-- 348  
 Db 304 LANGVIDS-DGNVIVTFDIVDNKENVANTIMPAYID--PENVKTGNTLTGIGT 358  
 Qy 349 SYNKNTIWEYORPNRNPANLGSMTNTDKTNTKNTVEQTYINPLRSAKETNY---- 402  
 Db 359 NTASKTIVLDEYKQFHNLISKCTIDQIDKTNKTYRQTYVNP----SGDNVLPALT 413  
 Qy 403 -NTLSGNGDEGSTIIDSTIKVYVGNDNLPSNRIVYSEVEDVNDYAQLGNNNDV 461  
 Db 414 GNILPNTKSNALIDAQNPKVYRV--DNANDLSEYYVVPNSDFEHNUTNOVRISPFPANCY 472  
 Qy 462 NINF---GNIDSPYIYKISKYDPNKKDITYTQOTVTMOTNTIYEYTGEP--RTASYDNT 515  
 Db 473 KVESEPTDDQPIITRYIVVNGHIDPASTG----DLAISRSTFGYDSFLWRMSWNE 526  
 Qy 516 TAFSSSSGGQQG-DLP--PEBKTYKGDY--WVEDVDKD-GIQNQNDN 556  
 Db 527 WAFNNGSGSGDGGIDKPVVPEQDPGEIEPIPEDSDSDPGSDGS 573  
 RESULT 9  
 90070  
 Species: Stephylococcus aureus (strain N315)  
 Species: Stephylococcus aureus  
 ;Accession: F90070  
 ;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 ;Accession: F90070  
 ;Status: preliminary  
 ;Gene: CIRB  
 ;Reference number: A89758; MUID:21311952; PMID:11418145  
 ;Accession: F90070  
 ;Status: preliminary  
 ;Molecule type: DNA  
 ;Residues: 1-877 <KUR>  
 ;Experimental source: strain N315  
 ;Cross-references: GB:BA000018; PID:913702588; PIDN:BA43728.1; GSPDB:GN00149  
 ;Accession: S19702  
 ;Status: preliminary  
 ;Molecule type: DNA  
 ;Residues: 1-960 <JCB>  
 ;Cross-references: EMBL:X62992; NTID:949040; PIDN:CAA44726.1; PID:9581562  
 ;Keywords: fibronectin binding

RESULT 10  
 S19702  
 fibronectin-binding protein B - *Staphylococcus aureus*  
 C;Species: *Staphylococcus aureus*  
 C;Sequence: S19702  
 C;Accession: S19702  
 R;Joensson, K.; Signaes, C.; Mueller, H.P.; Lindberg, M.  
 Bur. J. Biochem. 202, 101-1048, 1991  
 A;Title: Two different genes encode fibronectin binding proteins in *Staphylococcus au*  
 A;Reference number: S19702; MUID:92111475  
 A;Accession: S19702  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-960 <JCB>  
 A;Cross-references: EMBL:X62992; NTID:949040; PIDN:CAA44726.1; PID:9581562  
 C;Keywords: fibronectin binding

Query Match 12.2%; Score 376; DB 2; Length 940;  
 Best Local Similarity 23.4%; Pred. No. 5.6e-09; Mismatches 217; Indels 124; Gaps 22; Matches 138; Conservative 110; N mismatches 217; Indels 124; Gaps 22;

Qy 42 GIEKRSBRDTESTINNDEATFLQTKPQDNWHLTREVKESSVESSNSSIDTAQ--- 97  
 Db 30 GOKEEARASEQNNTVEES-----GSSATESSKASTQTQTTINVNNTIDEQSYA 78  
 Qy 98 ---OPSHT-TINREESVQ---SDNVEDSHUSDFANSKIKESNTSGKEENTIEOPNKVK 150  
 Db 79 TSTEQPQSQSTQVTEERPKVQAPKVETRY-DLPSEKVADEKETGTQVD-TAQPSNS 135  
 Qy 151 EDSTSQPSGTMNIDKIKISNODELLNL-PINEKENKARPLSTSQAQSSIKRIVTQNLAEO 210  
 Query Match 13.1%; Score 405.5; DB 2; Length 877;  
 Best Local Similarity 24.4%; Pred. No. 2.8e-10; Mismatches 210; Indels 153; Gaps 23; Matches 144; Conservative 82; N mismatches 210; Indels 153; Gaps 23;

|                                                                                                                                                                                                                                                   |                                                                        |                                                                            |                               |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------|----------------------------------------------------------------------------|-------------------------------|
| Db                                                                                                                                                                                                                                                | 136                                                                    | E-----IKPERRQKSTDVIAVEA                                                    | 153                           |
| Qy                                                                                                                                                                                                                                                | 211                                                                    | -----GSNNVLHLKVQDOSITEGYDSEGVIAKAHDENLIVYDVFEDDKVKGSDT                     | 261                           |
| Db                                                                                                                                                                                                                                                | 154                                                                    | EVVEETKATGFDVTNKVEVBGSETVGHKQDNTVVNVPHNAEVRUTLYKWFGEIGIRAGDY               | 213                           |
| Qy                                                                                                                                                                                                                                                | 262                                                                    | MTVIDKNTVPSDLTSFTIRKIKDNSGEITATGTYDNKNCITYFTDYDKYENKAH                     | 321                           |
| Db                                                                                                                                                                                                                                                | 214                                                                    | FDFTLSDNVETHGISLRKVKFVEIKSFTDQMVATGEIGERK-VRYFKEKYYQEKKLTAE                | 272                           |
| Qy                                                                                                                                                                                                                                                | 273                                                                    | LSLNLFIDPTVTKONQ-NVEVKLGETVKIFNQYLGVDNGVTAN----GRID                        | 326                           |
| Db                                                                                                                                                                                                                                                | 379                                                                    | TKNHT--VECTIYINPLRSAKETVNNSINGDEASTIIDSTIJKVKGDNQLPDS                      | 435                           |
| Qy                                                                                                                                                                                                                                                | 322                                                                    | LKLTSYDLSKVPNNNTKLVEYKTLASSVNLKTYVEY--OPRNENRNTANLQSMFTND                  | 378                           |
| Db                                                                                                                                                                                                                                                | 327                                                                    | TLNKVGDGFHFAVYMPKNNSL--SSVTGQVTKGNPKGVNPPTVKVYKHGSDLAES                    | 384                           |
| Qy                                                                                                                                                                                                                                                | 436                                                                    | --NRIVDSEVEDVTNDYAOGLNNNDVNINFGNIDSP--VIKVISQYDNNKDDYTQ                    | 491                           |
| Db                                                                                                                                                                                                                                                | 440                                                                    | --LEFOTHLFGVNYYNTSNTJWKNGYAFYNNAQDGDKLKEPITEHSTPIELPFKE                    | 497                           |
| Qy                                                                                                                                                                                                                                                | 539                                                                    | DYWWEDVKDOIQINTNEKPLSNLVLT---YPDGHSKSVRDED                                 | 582                           |
| Db                                                                                                                                                                                                                                                | 498                                                                    | PPVKEHLTGTEESNDS-KPIDEFEYHTVAVBGAEGT--IETEDD                               | 542                           |
| RESULT                                                                                                                                                                                                                                            | 11                                                                     |                                                                            |                               |
| Q90053                                                                                                                                                                                                                                            |                                                                        | hypothetical protein fnbb [imported] - Staphylococcus aureus (strain N315) |                               |
| C;Species:                                                                                                                                                                                                                                        |                                                                        | Staphylococcus aureus                                                      |                               |
| C;Date:                                                                                                                                                                                                                                           | 10-May-2001                                                            | #sequence_revision 10-May-2001 #text_change 22-Oct-2001                    |                               |
| C;Accession:                                                                                                                                                                                                                                      | G90053                                                                 |                                                                            |                               |
| C;Date:                                                                                                                                                                                                                                           | 10-May-2001                                                            | #sequence_revision 10-May-2001 #text_change 22-Oct-2001                    |                               |
| C;Accession:                                                                                                                                                                                                                                      | H90053                                                                 |                                                                            |                               |
| R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ouchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. |                                                                        |                                                                            |                               |
| Lancet                                                                                                                                                                                                                                            | 357,                                                                   | 1225-1240, 2001                                                            |                               |
| A;Title:                                                                                                                                                                                                                                          | Whole genome sequencing of meticillin-resistant Staphylococcus aureus. |                                                                            |                               |
| A;Reference number:                                                                                                                                                                                                                               | A89758;                                                                | MUID:21311952; PMID:11418446                                               |                               |
| A;Accession:                                                                                                                                                                                                                                      | H90053                                                                 |                                                                            |                               |
| A;Status:                                                                                                                                                                                                                                         | preliminary                                                            |                                                                            |                               |
| A;Molecule type:                                                                                                                                                                                                                                  | DNA                                                                    |                                                                            |                               |
| A;Residues:                                                                                                                                                                                                                                       | 1-1038 <KUR>                                                           |                                                                            |                               |
| A;Experimental source:                                                                                                                                                                                                                            | strain N315                                                            |                                                                            |                               |
| C;Genetics:                                                                                                                                                                                                                                       |                                                                        |                                                                            |                               |
| C;Gene:                                                                                                                                                                                                                                           | fnbb                                                                   |                                                                            |                               |
| Query                                                                                                                                                                                                                                             | Match                                                                  | 10.6%                                                                      | Score 326; DB 2; Length 1038; |
| Best Local Similarity                                                                                                                                                                                                                             | 23.1%                                                                  | Pred. No. 8.8e-07;                                                         |                               |
| Matches                                                                                                                                                                                                                                           | 139;                                                                   | Conservative 102; Mismatches 215; Indels 146; Gaps 30;                     |                               |
| Qy                                                                                                                                                                                                                                                | 42                                                                     | GIEKRSEDRTESTVNNDENATFLQKTPQN-----THLTLTEEVKESVSESSNSIDTAQ                 | 97                            |
| Db                                                                                                                                                                                                                                                | 30                                                                     | GQDKREAASEQKTTEVEEN-----GNSADNKTSQTATVNHHIEQSINYAT-TE                      | 82                            |
| Qy                                                                                                                                                                                                                                                | 98                                                                     | QPSIT-TREESTQTSNDVEDSHSFANSKTKSNTSGKERTIEOPNPKRSDTS                        | 156                           |
| Db                                                                                                                                                                                                                                                | 83                                                                     | QPSNATQVTEAPRVAQ-----APOTAQPNVTEKE--EPR-QVK--TT                            | 125                           |
| Qy                                                                                                                                                                                                                                                | 157                                                                    | QPSGTINIDEKISQDELLNLPINEYENK-----ARPLSTSAQPSIKRVTNQLA                      | 208                           |
| Db                                                                                                                                                                                                                                                | 126                                                                    | QP-----QDNSGNQRQVDTLPKKTQGQTETQEVAPRTASESKPRYR-SADVAEA                     | 178                           |
| Qy                                                                                                                                                                                                                                                | 209                                                                    | EQGSNNVLHLKVQDOSITEGYDSEGVTKA-----HDAENLTYDVFEDDVVKSGD                     | 260                           |
| Db                                                                                                                                                                                                                                                | 179                                                                    | KEASDVSE-VKGTD--VSKVTVESGSIEAQPQNKVPHAGORVVLKFKADGLRGD                     | 235                           |
| Qy                                                                                                                                                                                                                                                | 261                                                                    | TMTVDIDKNTVPSDUDTSDFTIPKDKNS---GFIATGTYDNKNCITYFTDYDVKY                    | 315                           |
| Db                                                                                                                                                                                                                                                | 236                                                                    | YFDFTLSNVNTYGVSTARVPEIKINGSYVMATGILNG-----NTRYTFNEHK                       | 288                           |
| Qy                                                                                                                                                                                                                                                | 316                                                                    | ENIKAHKLKLTSYDKVKVN-----NTKLDVEVKTLASSVNLKTYVEYORPNENRANL                  | 370                           |

Db 289 VEVVANLEINLFIDPKTVQSNQGQKINSLNGB-----ETEKTIPVVYNGPGVNSNTNV 342  
 Qy 371 QSMFTNIDTKNHTWQTYIYINPLRSAKETNNVNSIGNDGEGSTIIDSTTIKVY-VGDN 429  
 Db 343 NOSIETENKESNKFTHAYIKPQMGNSNT-PSVTGULTEGENLNLAGSOPTVKVYEVGKK 401  
 Qy 430 QNLPSNRIV---DYSEYEDVNNDYAQLG--NNNDVNINFGNIDSPYIIVKSYDPN 483  
 Db 402 DELPOS-WYANISDTNFKDFKEMKGKLSDQNGSYSLNLDKIDKTVIHYTGEVLOG 459  
 Qy 484 KPYTTIQLQTVMQTTNEYTCAERTASYNTTAFSISSGQOGGLPEKTKIGDYWE 543  
 Db 460 SDQV-----NFRTELYG-----PERAYR-SYYVY- 483  
 Qy 544 DVDKDG-IONTNDNEKEPLSNVLVLTYPDGTSKS -VRTEDEGKX-----QFDGV 590  
 Db 484 ---GGYELTJWDN----GLVIJSNKADGNGKNGQITODNDEFYKDPAKGTMSQVDK 534  
 Qy 591 QV 592  
 Qy 535 QI 536

RESULT 13  
 A32192  
 fibronectin-binding protein - *Staphylococcus aureus*  
 C;Species: *Staphylococcus aureus*  
 C;Date: 31-Jul-1989 #sequence\_revision 31-Jul-1989 #text\_change 16-Feb-1997  
 C;Accession: A32192  
 R;Signaes, C.; Raucci, G.; Joensson, K.; Lindgren, P.E.; Anantharamaiah, G.M.; Hoeoek, M.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 699-703, 1989  
 A;Title: Nucleotide sequence of the gene for a fibronectin-binding protein from *Staphylococcus aureus*  
 A;Reference number: A32192; MUID:89098998  
 A;Molecule type: DNA  
 A;Accession: A32192  
 A;Status: Preliminary  
 A;Residues: 1-1018 <STC>  
 A;Cross-references: GB:J04151  
 C;Keywords: fibronectin binding

Query Match 9.8%; Score 304; DB 2; Length 1018;  
 Best Local Similarity 21.2%; Pred. No. 7.5e-06;  
 Matches 125; Conservative 121; Mismatches 241; Indels 104; Gaps 26;

Qy 42 GIERNSEDRTESTNNVDENEATFLQKTPODN---THLTHEEEVREKSSVESSNSIDTAQ 97  
 Db 30 GQDKKAAMSEOKTTIVEEN----GNSATDNKYSSETIOTATNNHIEETQSINYAV-TE 82  
 Qy 98 QPSHTT-INREE---SVQTSNDVEDSHVSDFANSKIKESNTESKEENIEQPNVKEDS 153  
 Db 83 OPSNATOVTEEAQAKAVQAPOTAQPANTIEVKEEVKE-----EAKPOKEMT 130  
 Qy 154 TTSPGSG---YTNIIDEKLSQNDETLNLNPINEYENKARPSTSIQFSIKRT----V 203  
 Db 131 QSDONSGDORQDVITPKKATQDAETQV---EVAQPTTAESKERVRSADAEEKA 186  
 Qy 204 NQLAEQGSNNVNHLLKVTQDOSTBEGDSEGVRKAHDAAENLYIVTFEVDK/RSGDTWT 263  
 Db 187 SNAKVETGDTVSKVTEVERGSI EGHNNTNKV EPHAGORAVLKYLKFFENGHQGDFD 244  
 Qy 264 VDTIKNTVSDLTSFTTICKDMS---GEIATGTYDNKNQIYTFTDYKVENI 318  
 Db 245 FTLSNNVNTHGVSTARKVPEIKNGSVVMTGEVLEGG-----KIRYIFTNDIEDKV 297

RESULT 14  
 T30856 F2 - *Streptococcus pyogenes*  
 C;Species: *Streptococcus pyogenes*  
 C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 11-May-2000  
 C;Accession: T30856  
 R;Jaffe, J.; Natanson-Yaron, S.; Caparon, M.G.; Hanski, E.  
 Mol. Microbiol. 21, 373-384, 1996  
 A;Title: Protein F2, a novel fibronectin-binding protein from *Streptococcus pyogenes*,  
 A;Reference number: Z20907; MUID:97011581  
 A;Accession: T30856  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-1039 <JAF>  
 A;Cross-references: EMBL:U31980; NID:91654115; PID:91654116; PID: AAC44522.1  
 C;Genetics: A;Note: PRTF2

Query Match 7.7%; Score 239; DB 2; Length 1039;  
 Best Local Similarity 22.6%; Pred. No. 0.0046;  
 Matches 93; Conservative 79; Mismatches 168; Indels 72; Gaps 18;

Qy 224 SITEGYDSEEGVIAHD---AENLYDVTFFDDKVKS---GDTMVTDIDKNTVSDL 275  
 Db 38 SVSKVYGEOEKTSNSADFYRNHAAYKMSFELKOKDKSETINPGDTFVQLQDRRLNPFGI 97  
 Qy 276 TDSTPIK-IDKDSGEIATGTVTDNKQIQTYPDVKYKENIKAHKLTSTIDSKVP 334  
 Db 98 SQD--IPKLYDSENNSPLAIGKVDKATHOLITYFTNYLAGDKWVSAELSFLLENKEV 155  
 Qy 335 NNNTKLDVKEYKTLASVNVKTTIVYQRFNE-----NRTANLQSMFTNIDTKNHE 385  
 Db 155 ENTISDRFSTISQEQITKGTVWLYNGESTKESNVTNGLSNNGGSTE SYWTEGFV 215  
 Qy 386 QTIVINPLRYSAKETNNVNS-----NGDEGSPITIDS-TIKVYKVGDNONLPSNR 437  
 Db 216 WYVIVNPNTNIPVAVLNWGFAKRTAQGENDNSLVSSAQLGDIYEVPHNRLPTSYG 275  
 Qy 438 IYDSEYEVITNDIYQI-----GNNNDVING-NID-SPYIKVISKYDNKDDTT 489  
 Db 276 V-DISRL-NLRKDLKEALKLPGOSTOGANKRKLRIDGENLOGKAFVVKVKGADOSKE-- 330  
 Qy 490 IQVTMOTINETT-GFRT-----ASYNTIAFSISSSGCGQ-----DLPEKT 534  
 Db 331 -----LIVDHOHSNNWSKYLPRNSHVSFTNLIALPKSGSGSTSRFTPSITVNL 386  
 Qy 535 YKIGDVWEDVKDGI-----QNTNDNEKPL--SNVLVLTYPDGTS 574  
 Db 387 KRVQOLRKFKVSTDNVPUFBAAFLRSSNGNSQLEASNTQGEBIFKDLTS 438

RESULT 15  
 T30290 AAS surface protein - *Staphylococcus saprophyticus*  
 C;Species: *Staphylococcus saprophyticus*  
 C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 02-Sep-2000  
 C;Accession: T30290  
 R;Heil, W; Meyer, H.G.W; Gattermann, S.G.  
 Mol. Microbiol. 29, 871-881, 1998

A; Title: Cloning of aas, a gene encoding a *Staphylococcus saprophyticus* surface protein  
 A; Reference number: 220809; MVID:90389318  
 A; Accession: T30290  
 A; Status: Preliminary; translated from GB/EMBL/DBJ  
 A; Molecule type: DNA  
 A; Residues: 1-463 <HEL>  
 A; Cross-references: EMBL:AJ000007; NID:e1295629; PID:e1295630; PID:CAA0852.1  
 A; Gene: aas

Query Match Similarity 7.3%; Score 225; DB 2; Length 1463;  
 Best Local 143; Conservative 105; Mismatches 263; Indels 172; Gaps 33;  
 Matches 143;

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| Qy | 8   | SSDEEKNDVNNNQST-----NTDDNNQTIKEETNNYDIEKRSRDRTESTT--         | 55  |
| Db | 180 | NDENNEATFLQKTPDNTH-----LVE--ERVKESSVESN--SSIDPQQPSH          | 101 |
|    | 56  | NAVSSNEDVASSDVQDGTHSDDNASDDLTQDQNEVAQNDKAETSNEVDYASSDVQDDTH  | 299 |
| Qy | 240 | TTIN-----REESTQSDNVEDSVDFANSKIKESNESG-----KEENIEQPN-         | 147 |
| Db | 102 | KEENIEQPN-----REESTQSDNVEDSVDFANSKIKESNESG-----KEENIEQPN-    | 147 |
|    | 300 | SDANASDVADNESETONDWAESSENNEDDVASSDVQDDTHSDANASDDYQDNESETOND  | 359 |
| Qy | 148 | --KVEDSTS--QPSGYNIDEKISQNQDELLNLPINEYENKARPLSTT              | 192 |
| Db | 360 | KAETSNEVDYASSDVQDDTHSDANASDIQDNEVAQNDKA-----ETSEDVASS        | 411 |
| Qy | 193 | SAQPSKIKRVTVNQLAEGQSNVNHLIKVT--DOSITEGDDS--EGVIK-AHDENLI     | 245 |
| Db | 412 | DKQDDTHSDANASDIQDNESETQDDKATSKEEDDVVSNDQDDNAKVSNIIKEASTAENKV | 471 |
| Qy | 246 | YDVTF--EVDKVKSQDTM-TVDIDKNTVPDLDSFTPKIKONSGEIJATGIDNN        | 301 |
| Db | 472 | QPATFSAKVTPLKRVATTSANTAVTRSAVTKEATRAALPKY-----S              | 515 |
| Qy | 302 | KQITVFTDKVVKYENIKA--HLKLTSYIDSKVFPNNNTKLDVVKTAISSLVNTKTE     | 358 |
| Db | 516 | YQRPNEERTANLQSMTNTDKHTVEQTYINPLRYSAKETNVNISNGDEGSTIIDD       | 572 |
| Qy | 359 | YQRPNEERTANLQSMTNTDKHTVEQTYINPLRYSAKETNVNISNGDEGSTIIDD       | 418 |
| Db | 573 | INYMKNYT--SAFVHAYDGRRIETANTDYLAWGA-----GPOANDRF              | 615 |
| Qy | 419 | TIKVVKVKGDNQNLPSNRITYSEVEDVNDYQGLNNINDVNINFGNIDSPYI          | 478 |
| Db | 616 | IHWELVHVTHDYDSFARS--INNYADYA-ATNLQYYGLVPD--SAEYDGVTWTHQAVS   | 669 |
| Qy | 479 | KY-----DPN-----KDDYTICQVTMOTTINETYGEERTASYDNTIAFST-          | 520 |
| Db | 670 | NYLGSSDHSPHGVLGAHNNTSYDLEDLIVELYLKTTG-----QAAWGTUSSGSGT      | 721 |
| Qy | 521 | -----SSGQGQ-GDLPEK--TYKIGDYWEDVKGQIQTNDNEKPLSNVLUVTLYPDGT    | 573 |
| Db | 722 | GTGGSGSGSGNGTTPSKSGVVK-----TENNOVGRINK---NDGLYTIVDQKG        | 770 |
| Qy | 574 | SKSVRHDDED-----GKTOF                                         | 587 |
| Db | 771 | KKTDRVQNLTKWTKSATLGKEQY                                      | 793 |

Search completed: July 30, 2002, 10:31:29  
 Job time: 154 sec







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 CC or send an email to license@isb-sib.ch).  
 DR EMBL: U39712; AAC1534.1; -;  
 DR ENB1: U02261; AAD12527.1; -;  
 DR TIGR: MG312; -;  
 KW Cytadherence; Structural protein; Complete proteome.  
 SEQUENCE 1139 AA; 130531 MW; 0011D328C3BD856 CRC64;

Query Match 6.5%; Score 19.5.; DB 1; Length 1139;  
 Best Local Similarity 21.0%; Pred. No. 12; Mismatches 225; Indels 161; Gaps 27;  
 Matches 129; Conservative 98; MisMatches 225; Indels 161; Gaps 27;  
 OY 1 HHHHHHPPSSDEPEKENDVNNHQ-SINTDDNMQI--IKKEFINNYDG-----IE 44  
 Db 578 HHEELKPVAEEQNQYQGFDQVOANLNDNNIEEIQPTAEKETTDFESKQAQVWDSYOLPID 637

45 KRESDRT----ESTINVDNEATFLQKTPQDNTNLHTEBEVKESS----SVESSN-- 90  
 Db 638 TDQDOTTFSSEFQPTVQEDFQDNSEVNDQFKBTKPYLESFNKDVVERNSYN 697

OY 91 --SSIDTAQQPSHTTINREEVVOTSDNVEDSHVSDFANSKIKES---NTESGKENTIE 144  
 Db 698 NLQKEDIOSDNKIIITKSSPQIPPTLPISFVSNRIEYKVETALDNBESQQEQITI- 756

OY 145 QPNKVEDSTTSQPSYTNIDE-KLSNQ---DELLNPINEVENKARLSTISAQPSI 198  
 Db 757 --NSTEDSKTLAKTSLVOLQOINSLNQSVITVSERVLKKDDLTINTVNSEDQPKI 814

OY 199 KRVTVNQLAEGGSNNVNLHKVTDQSITEGYDSECVIKAHDENAENLYDVFVDDVK 258  
 Db 815 EVFVKAKEPYEEHSITONKOSVEDSELDNNKKDL-----YKILSELK 860

OY 259 GD-TMVKDIDKNTVPSDLTDSFTIPIKDNGSEIATGTVDNNKQITYIFTTYDKEN 317  
 Db 861 GEJNPNINFO-----AIIQMDYQMSVKQSPFHNLDFNTVYN 898

OY 318 -----IAKHL--KLTSYIDKSK--VPNNTK-----LDEYKTA 347  
 Db 899 QISERVLLIKKELQSELBSRLIDQENLNQVFNANKLTQKEEMIRSLASDAIAYKPS 958

OY 348 -----LSSVNKTIVYORPNTNTANQSMFTNDTQNHTVQDTI-----Y 389  
 Db 959 NSYEQLQKSGETMRHVORATT-----ENKEKIESIQLSKQLKTVYNSCETIMNNINKL 1013

OY 390 INPLRSAKETVNNSNGD-----EGSTIIDSTIKVYKGDQNQLPDSRIYD 441  
 Db 1014 DNTLRPKKEEDPLLSNFSDWTQDNGLVEPRQMLDD--LIDFSNFDFN---ISSEQLDD 1067

OY 442 SEYEDY-TNDYYAQLGNNDVNINFNGNIDSPTYIYKISKVDPKNDYTTIQTWT--- 495  
 Db 1068 FIYENMDRNIDFEPEGFND---FVIDAK-VMDMSAFSAVNDLIDETLVPDTSNFSS 1122

OY 496 -MOTTNEYGYCF 507  
 Db 1123 LIDEDLFESSGDF 1135

RESULT 5  
 YNJB\_CAEEL STANDARD; PRT; 918 AA.

ID YNJB\_CAEEL STANDARD; PRT; 918 AA.

AC P34487; 1:  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.  
 GN F59B2.12.  
 CAenorhabditis elegans.

OCC Eukaryota; Metacoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pecloderinae; Caenorhabditis;  
 OX NCBI\_TaxID=6239;

RN [1] SEQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BRISTOL N2;  
 CC MEDLINE=94150718; PubMed=7905398;  
 RX Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser N.,  
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
 RA Johnston L., Jones M., Karshaw J., Kirsten J., Laisteller N.,  
 RA Latrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkenen R.,  
 RA Sims M., Smaldoon N., Smith A., Smith M., Sonnhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Spratt J.,  
 RA Wohldman P.;  
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
 RL Nature 368:32-38(1994).

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 or send an email to license@isb-sib.ch).  
 CC  
 DR EMBL: Z11505; CAA77581.1; -;  
 DR PIR: S31132;  
 DR Wormpep: F59B2.12; CB01024.  
 DR Wormpep: F59B2.12; CB01024.  
 KW Hypothetical protein.  
 SQ SEQUENCE 918 AA; 96560 MW; B464FD86B14945DB CRC64;

Query Match 6.4%; Score 197; DB 1; Length 918;  
 Best Local Similarity 20.5%; Pred. No. 0.12; Mismatches 91; Indels 176; Gaps 27;  
 Matches 142; Conservative 91; MisMatches 91; Indels 176; Gaps 27;

OY 2 HHHHHHSS-----DEEKNDVNNNQSNINTDDNQI----- 33  
 Db 74 HKGHROSSGSSNTHSLTVGADGNNTENSEKKGYKSYKVDANEWTIKSADGVI 133

OY 34 -----REBTENNNDGIEKRSEDRTE-----STTYDENEAT-----TFLQKT 68  
 Db 134 ETGKSHNKSDDASSY-GLERSSKTYADKNQTMSSNTKINNOSSRALSADEGNEFVNQ 192

OY 69 PQDNTL-----TEEVKESSEVSSNSIDPAQPSTTINREEVQTSDN-VEQS 119  
 Db 193 NADGTFLNRNTHGKNTDEHSHVNLDENADMSIG-ADTGHNTRURKGSGYGDHNAASDA 251

OY 120 HVSDFANSKIKESNTESGKEENTIEQPNKYKEDSTSQPSGYTNIDEKISNQDELNLPI 179  
 Db 252 H-----SNEFLDAQGNKNSQNYKAASAG---SNADFE-SNLESKNAQG 295

OY 180 NEYENKARPLSTS-----AQPSIKRVN-----OLAAEQGSNNVNLHKVTDOSITEG 228

OY 296 TSMSTGNFNNTSDKATAEVEVMSKVNNADGTSSMEASHAGSNSSKINSASGSSDLS 355

OY 229 YDSECYVKAIDAENLYDVFEDDKVSKSDTMVTDIK----- 268  
 Db 356 MVGPNG-IKSISNTDN--VALDENQSGASISBOQINGQNSLINESSTESGRKAESR 412

OY 269 NTVPSDLTDSFTIPIKDNGSEIATGTVDNNKQITYIFTYDKYKENIAKHLKTSYI 328  
 Db 413 NNTAADTLSVDANGFVSSHSKHSAGTSLSDENHNTAQASVDEBHGNNKHNSDGTYSR 472

OY 329 DKSKVNNNTLDEVEKTA---LSSVN-----KTIIVEVQRPNENRANTLQSKFTNID 378  
 Db 473 NKKTGFGNSMSASIKNADGTMQSVNQVKNDTRNRYEAKSALKENHEKNSDGTFKD-- 530

OY 379 TKNHTVEQTIVINPLRSAKETVNNSNGDSEGSTDTEITKVKVQDNLQNSDNTI 438

Db 531 -----ESKGNSRNV-RDGGGSNLAVGSKVSGGGVSSNETTASSN-A 571





OS Candida albicans (Yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
 OX NCBI\_TaxID=5476;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ACC 10261;  
 RX MEDLINE=85525638; PubMed=85525638;  
 RA Gale C., Finkel D., Tao N., Meinke M., McClellan M., Olson J.,  
 RA Kendrick K., Hostetter M.;  
 RT "Cloning and expression of a gene encoding an integrin-like protein  
 in *Candida albicans*.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:357-361(1996).  
 CC -I- FUNCTION: COULD PLAY A ROLE IN ADHESION AND IN STE12-INDEPENDENT  
 MORPHOGENESIS.  
 CC -I- SUBCELLULAR LOCATION: CELL-SURFACE OF THE BLASTOSPORES.  
 CC -I- SIMILARITY: SOME, WITH INTEGRIN ALPHA CHAINS.  
 CC -I- SIMILARITY: CONTAINS 1 PH DOMAIN.

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CC EMBL: U5070: AAA98019\_1; DR InterPro: IPR01849; PH: Pfam; PF0169; PH: SMART; SP00233; PH: PROSITE; PS50003; PH\_DOMAIN; KW Cell adhesion; Glycoprotein; DOMAIN 1527; 1636; FT SITE 1149; 1151; FT SITE 1150; 50; FT CARBOHYD 154; 215; FT CARBOHYD 223; 265; FT CARBOHYD 268; 285; FT CARBOHYD 289; 305; FT CARBOHYD 314; 446; FT CARBOHYD 446; 583; FT CARBOHYD 638; 670; FT CARBOHYD 670; 691; FT CARBOHYD 817; 838; FT CARBOHYD 841; 1018; FT CARBOHYD 1082; 1100; FT CARBOHYD 1103; 1113; FT CARBOHYD 1200; 1571; FT CARBOHYD 1593; 95; FT DOMAIN 283; 286; FT DOMAIN 1283; 1592; FT DOMAIN 1651; 1660; SQ SEQUENCE 1664 AA; 187859 MW; BA2EF0DC8196790 CRC64;

Db 138 DKVNENHAPTYINTSPNKSIMKKATPKASPKKAVFTVNPPIHYP--DNRVEEEDQSQ 195  
 Qy 56 NVDENEAETLQTKTQDNTILTEEVKESSSVESSNSSIDTAQPSHTT-----INRE 108  
 Db 196 KEDSVEPPLIQ-----HCKDPDSOFNYSDEDTNASVPTT-PPLHTRTPFAQLNN 247  
 Qy 109 SVQTSNDVESHVSD-----FANSKIE-----SNTESGKREENTFQPQNKVEDST 155  
 Db 248 EV---NSPEALTDMLKRENTSNLSUDEKVNLSPINNNNSKNSDMSHQ---N 299  
 Qy 156 SOPSCTYTIDEKTSNQDELNLNPINEYENKARPL-STTAQPSIKRVTVNLAEGQSY 214  
 Db 300 LQDASKNKNTENIHNLSPALKAPKNDIEN--PLNSLTNDISLRSSGSSOSLSLRND 356  
 Qy 215 NHLIKV--TQSITEGYDSEGYTIKAHDAAENLYDVFEVDKVKSGDPMVTDKNV 271  
 Db 357 NRVLSEVPGPSPKKVNGPLSLNDGIGKFSDD-----EVVESL 392  
 Qy 272 PSDLT-DSFTIPKID---NSGEIATGYDKNNKOIYTTFDVKYENIKAH--- 321  
 Db 393 PRDLRSRKETTKEAPEHNENFADNSTNTNG-QLVSSDHDLSFDNSYNHTEQS 451  
 Qy 322 -LKUTSYIDSKVPPN-----NTKLDVYKTTALSSYWK 353  
 Db 452 ILNLNSASQSQISINALEKQRQTOEQTQAEEPEEETFSNDNIVKQEPKSNEFLVKV 511  
 Qy 354 TITVYKRPENRTANLQNSFTNIDTKNH-TVEOTIYVHLRYSAKENWNIS----- 406  
 Db 512 TIKKEPVSAETIKAKPREFSSIRIKRNEDIAEPADIHKRKENAENSHEWDTALLKA 571  
 Qy 407 -NGDGSTIDTDSTIKV-KVKGDNQNLPDSNRVYDVSYEDVNDYQQLGN--NDV 461  
 Db 572 LNDDESESTDTONSTMSIRFHSDWKLDNSD---GDRED--NDDLSRFPEKSDILNDY 625  
 Qy 462 N-----INFGNIDSPYIYKVISVKYDPNKKDDYTITQVTMOTTINEVYGEFR----T 509  
 Db 626 SQTSNIIGDXYGSSENSEITTKTLA--PPRSNDNUKRSLEDPANNESLQQQLEVPH 682  
 Qy 510 ASYDNTIAFSTSSGGOGDPDPEK---TYKIGDY-WWEIVDK 547  
 Db 683 KEDDSILANSNSIA-----PPEELTLPVVEANDISSFNNDVTK 719  
 RESULT 9  
 EBL-PLAFC ID EBL-PLAFC STANDARD: PRT: 1435 AA.  
 AC P19214; DT 01-NOV-1990 (Rel. 16, Created)  
 AC P01-FEB-1996 (Rel. 33, Last sequence update)  
 AC 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Erythrocyte-binding antigen ERA-175.  
 OS Plasmodium falciparum (isolate Camp / Malaysia).  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OC NCBI\_TaxID=5835;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90377259; PubMed=2204835;  
 RA Sim B.K.L.  
 RT "Sequence conservation of a functional domain of erythrocyte binding  
 antigen 175 in Plasmodium falciparum.";  
 RT Mol. Biochem. Parasitol. 41:283-298(1990).  
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 DR EMBL: X52524; CAA36756.1; -  
 DR PIR: S11561; S11561.

Query Match 6.1%; Score 189.5; DB 1; Length 1664;  
 Best Local Similarity 20.4%; Fred. No. 0.49;  
 Matches 131; Conservative 105; Mismatches 236; Indels 171; Gaps 31;

Qy 15 DVINNNQOS--INTDDNNQIJKK-----BETNIVDGIERSERTESTT 55

|            |                                                                                                                                                                                                         |                                                                                                                                                                                                         |                      |                                    |                          |                                                                      |    |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------|------------------------------------|--------------------------|----------------------------------------------------------------------|----|
| KW         | Antigen.                                                                                                                                                                                                | 159                                                                                                                                                                                                     | 1104                 | ESSENTIAL FOR BINDING TO           | RT                       | chromosomal assignment, and expression of the M and A chain in human |    |
| FT         | DOMAIN                                                                                                                                                                                                  | 159                                                                                                                                                                                                     | 1104                 | ERYTHROCYTES.                      | RT                       | fetal tissues.",                                                     |    |
| FT         | VARIANT                                                                                                                                                                                                 | 1031                                                                                                                                                                                                    | 1031                 | E -> V (IN STRAINS FCR-3 AND ITG). | RL                       | J. Cell Biol. 124:381-394(1994).                                     |    |
| SQ         | SEQUENCE                                                                                                                                                                                                | 1435                                                                                                                                                                                                    | AA;                  | 167389 MW;                         | RN                       | [2]                                                                  |    |
| QY         | 8                                                                                                                                                                                                       | SSDREKNDVNNQSINTDDNNQI                                                                                                                                                                                  | KKEETWYDG            | ...IERSEDRTESTVNVDEN               | 60                       | SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.                            |    |
| DB         | 875                                                                                                                                                                                                     | NSDESEETVWNH-                                                                                                                                                                                           | -.....-ISRPSTINGGDGS | GSAWYBSSSSWNGLSDDRN                | 923                      | TISSUE=Placenta;                                                     |    |
| QY         | 61                                                                                                                                                                                                      | ENTFQKTPQDWTBLTBEV-                                                                                                                                                                                     | KESSVESSNS           | NSISDTAQOPSHTTINRESE               | 118                      | MEDLINE=97066955; PubMed=8910357;                                    |    |
| DB         | 924                                                                                                                                                                                                     | GDFIVFVQTDTAN                                                                                                                                                                                           | ...-EDVIRKENADKEDEG  | ADEERHSSESLSSPERKMTDNEG            | 979                      | Zhang X., Vuolleennaho R., Tryggvason K.;                            |    |
| QY         | 119                                                                                                                                                                                                     | SHVSDFRNASKRE-NTNESKE                                                                                                                                                                                   | KEENTIEOPKVKE        | DSTTSQFSGYTNIDE-                   | 166                      | "Structure of the human laminin alpha2-chain gene (LAMA2), which is  |    |
| DB         | 980                                                                                                                                                                                                     | NSLN--HEEVKEHTSNDSNVQOSGG                                                                                                                                                                               | GVNVMVEKELDTLEN      | PS-SSLDGEGKAHELSE                  | 1034                     | affected in congenital muscular dystrophy.";                         |    |
| QY         | 167                                                                                                                                                                                                     | -KISNODELLINP                                                                                                                                                                                           | INYEKNAKLRS          | TSAQPSIKRIVNQLAEQCSNVHLIKTDQSI     | 225                      | J. Biol. Chem. 271:27664-27669(1996).                                |    |
| DB         | 1035                                                                                                                                                                                                    | PNLSSDDDMNSNP                                                                                                                                                                                           | -----GPLDNTS         | -EHTTERISNEYKVNE                   | -----REDERTL             | [3]                                                                  |    |
| QY         | 226                                                                                                                                                                                                     | TEGYDIDSEGVIKAH                                                                                                                                                                                         | -----DAENLYDVTF      | EVDDKKVKGDTMTIDKNVTPVPSDITSF       | 279                      | SEQUENCE OF 1981-3110 FROM N.A., AND PARTIAL SEQUENCE.               |    |
| DB         | 1078                                                                                                                                                                                                    | TKEYEDT-VIKSHMRE                                                                                                                                                                                        | EDCGE                | -----ENSLSTVNDSEDAEARMKGND         | 1124                     | RT                                                                   |    |
| QY         | 280                                                                                                                                                                                                     | TIPIKIKONGSEIATGTYDNK                                                                                                                                                                                   | QKITYTFDVKYD         | YENIKAHLKTSYIKSKV                  | 339                      | RT                                                                   |    |
| DB         | 1125                                                                                                                                                                                                    | T-SEMISHNNSQHES                                                                                                                                                                                         | EDQOKNDMKTVGDLG      | LTHVON                             | -----EISVPIVGEIDEKKRESKE | 1179                                                                 | RA |
| QY         | 340                                                                                                                                                                                                     | LDEVYKALSSNKNTIVE                                                                                                                                                                                       | YKOPNERTANTQSM       | -FTNIDTKNKHVEQTYYIN                | 397                      | RA                                                                   |    |
| DB         | 1180                                                                                                                                                                                                    | IHKAEERERL                                                                                                                                                                                              | SHSTD---IHKTP-       | EDRNSNTLHLKDTRNEENERHLLTNQNI       | 1234                     | RA                                                                   |    |
| QY         | 398                                                                                                                                                                                                     | K--ETVNNSCNGD                                                                                                                                                                                           | ESTIIDDSTIKV         | YKVGDNQNLPSNR                      | YDSEYEDVNTNDIYA          | 454                                                                  | RA |
| DB         | 1235                                                                                                                                                                                                    | KIGFHTNMLNLDG                                                                                                                                                                                           | -----VSERSONHS       | HGNRQD                             | -----R                   | RA                                                                   |    |
| QY         | 455                                                                                                                                                                                                     | IKNNNDV-----N                                                                                                                                                                                           | NGNINNSPYIKV         | ISKVKD                             | -----PNKEDYTTOQQT        | 500                                                                  | RA |
| DB         | 1267                                                                                                                                                                                                    | GNSGNVNLMMNNNNNNN                                                                                                                                                                                       | ISRY                 | -----NLYDKKKLDLYEN                 | ENDSIT-KELIKK            | 1320                                                                 | RA |
| QY         | 501                                                                                                                                                                                                     | NHYTGFERTASDNTI                                                                                                                                                                                         | 516                  |                                    |                          | RA                                                                   |    |
| DB         | 1321                                                                                                                                                                                                    | NKCNEENISV                                                                                                                                                                                              | KYCDHMI              | 1336                               |                          | RA                                                                   |    |
| RESULT     | 10                                                                                                                                                                                                      |                                                                                                                                                                                                         |                      |                                    |                          | RT                                                                   |    |
| LMA2_HUMAN | ID                                                                                                                                                                                                      | LMA2_HUMAN                                                                                                                                                                                              | STANDARD:            | PRT;                               | 3110 AA.                 | RT                                                                   |    |
| AC         | P24043;                                                                                                                                                                                                 | 014736; 093022;                                                                                                                                                                                         |                      |                                    |                          | RT                                                                   |    |
| DT         | 01-MAR-1992 (Rel.                                                                                                                                                                                       | 21, Created)                                                                                                                                                                                            |                      |                                    |                          | RT                                                                   |    |
| DT         | 01-NOV-1997 (Rel.                                                                                                                                                                                       | 35, Last sequence update)                                                                                                                                                                               |                      |                                    |                          | RT                                                                   |    |
| DT         | 01-MAR-2002 (Rel.                                                                                                                                                                                       | 41, Last annotation update)                                                                                                                                                                             |                      |                                    |                          | RT                                                                   |    |
| DE         | Laminin alpha-2 chain precursor (Laminin M chain) (Merosin heavy chain),                                                                                                                                | (Laminin alpha-2 chain precursor (Laminin M chain)) (Merosin heavy chain),                                                                                                                              |                      |                                    |                          | RT                                                                   |    |
| DE         | Homo sapiens (Human).                                                                                                                                                                                   | Homo sapiens (Human).                                                                                                                                                                                   |                      |                                    |                          | RT                                                                   |    |
| GN         | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;                                                                                                                                                   | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;                                                                                                                                                   |                      |                                    |                          | RT                                                                   |    |
| OC         | Euksaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                                                                      | Euksaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                                                                      |                      |                                    |                          | RT                                                                   |    |
| OC         | NCBI_TAXID=9606;                                                                                                                                                                                        | NCBI_TAXID=9606;                                                                                                                                                                                        |                      |                                    |                          | RT                                                                   |    |
| RN         | [1]                                                                                                                                                                                                     | SEQUENCE FROM N. A.                                                                                                                                                                                     |                      |                                    |                          | RT                                                                   |    |
| RC         | TISSUE=Placenta;                                                                                                                                                                                        | TISSUE=Placenta;                                                                                                                                                                                        |                      |                                    |                          | RT                                                                   |    |
| RX         | MEDLINE=94124633; Pubmed=8294519;                                                                                                                                                                       | MEDLINE=94124633; Pubmed=8294519;                                                                                                                                                                       |                      |                                    |                          | RT                                                                   |    |
| RA         | Vuoleennaho R., Niissinen M., Sainio K., Byers M., Eddy R., Tryggvason K., Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K., Human laminin M chain (merosin): complete primary structure; | Vuoleennaho R., Niissinen M., Sainio K., Byers M., Eddy R., Tryggvason K., Hirvonen H., Shows T.B., Sariola H., Engvall E., Tryggvason K., Human laminin M chain (merosin): complete primary structure; |                      |                                    |                          | RT                                                                   |    |

|       |                                                                                                                    |
|-------|--------------------------------------------------------------------------------------------------------------------|
| DR    | EMBL; U66741; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66742; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66743; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66745; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66746; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66747; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66748; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66749; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66750; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66751; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66752; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66753; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66754; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66755; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66756; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66757; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66758; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66759; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66760; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66761; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66762; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66763; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66764; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66765; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66766; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66767; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66768; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66769; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66770; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66771; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66772; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66773; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66774; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66775; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66776; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66777; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66778; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66779; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66780; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66781; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66782; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66783; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66784; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66785; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66786; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66787; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66788; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66789; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66790; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66791; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66792; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66793; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66794; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; U66795; AAB18388.1; JOINED.                                                                                  |
| DR    | EMBL; M59832; AAC03215.1; -.                                                                                       |
| DR    | PRR; A35899; MNHMH.                                                                                                |
| DR    | PRR; P02468; 1KLO.                                                                                                 |
| MIM   | 1_6225; -.                                                                                                         |
| DR    | InterPro; IPR000561; EGF-like.                                                                                     |
| DR    | InterPro; IPR001886; Laminin_EGF.                                                                                  |
| DR    | InterPro; IPR00034; Laminin_B.                                                                                     |
| DR    | InterPro; IPR002039; Laminin_G.                                                                                    |
| DR    | InterPro; IPR001791; Laminin_G.                                                                                    |
| DR    | Pfam; PF00052; laminin_B; 2.                                                                                       |
| DR    | Pfam; PF00053; laminin_EGF; 15.                                                                                    |
| DR    | Pfam; PF00054; laminin_G; 5.                                                                                       |
| DR    | Pfam; PF00055; laminin_Nterm; 1.                                                                                   |
| DR    | PRINTS; PR00011; EGFLAMININ.                                                                                       |
| DR    | PRINTS; PD002082; Lamnt; 1.                                                                                        |
| DR    | PRINTS; PD00331; Laminin_B; 2.                                                                                     |
| DR    | SMART; SM00018; EGF_Lam; 14.                                                                                       |
| DR    | SMART; SM00001; EGF-like; 3.                                                                                       |
| DR    | SMART; SM00281; Lamb; 2.                                                                                           |
| KW    | Laminin EGF-like domain; Basement membrane; Extracellular matrix; Coiled coil; Glycoprotein; Signal; Polymorphism. |
| KW    | Laminin EGF-like domain; Cell adhesion; Repeat; Signal; Polymorphism.                                              |
| FT    | SIGNAL 1 22                                                                                                        |
| FT    | CHAIN 23 3110                                                                                                      |
| FT    | DOMAIN 23 286                                                                                                      |
| FT    | DOMAIN 287 343                                                                                                     |
| FT    | DOMAIN 344 413                                                                                                     |
| FT    | DOMAIN 414 468                                                                                                     |
| FT    | DOMAIN 469 517                                                                                                     |
| FT    | DOMAIN 518 527                                                                                                     |
| FT    | DOMAIN 528 723                                                                                                     |
| FT    | DOMAIN 724 756                                                                                                     |
| FT    | DOMAIN 757 806                                                                                                     |
| FT    | DOMAIN 807 864                                                                                                     |
| FT    | DOMAIN 865 917                                                                                                     |
| FT    | DOMAIN 918 966                                                                                                     |
| FT    | DOMAIN 967 1013                                                                                                    |
| FT    | DOMAIN 1014 1059                                                                                                   |
| FT    | DOMAIN 1060 1105                                                                                                   |
| FT    | DOMAIN 1106 1165                                                                                                   |
| FT    | DOMAIN 1166 1175                                                                                                   |
| FT    | DOMAIN 1176 1379                                                                                                   |
| FT    | DOMAIN 1380 1419                                                                                                   |
| FT    | DOMAIN 1420 1468                                                                                                   |
| FT    | DOMAIN 1469 1526                                                                                                   |
| FT    | DOMAIN 1527 1573                                                                                                   |
| FT    | DOMAIN 1574 2144                                                                                                   |
| FT    | DOMAIN 2145 228                                                                                                    |
| FT    | DOMAIN 2340 2321                                                                                                   |
| Query | 6.0%; Score 186.5; DB 1; Length 3110;                                                                              |
| Match | Best Local Similarity 19.9%; Pred. No. 1.3; Matches 142; Conservative 102; Mismatches 256; Index 215; Gaps 32;     |
| Qy    | 28 NNOQIKKEET-----NNYDGIEKRSEDRTTESTPNVDENEATFLOKTPODNTLHTE 78                                                     |
| Db    | 1693 NEKAIRNLNETIGTGRDFAERFNLEGQK-----EIDOMIKELRKULETOQIAED 1742                                                   |
| Qy    | 79 EVKESSESVESSNSNNSIDTAQPSHTIN--REESVQTSNDVEDS-HVSDFANSKIRESN- 133                                                |
| Db    | 1743 ELVAABALLKKVKKLFGESRGENEMEKDLREKLADYBKVKYDWDLLREATDKIREANR 1802                                               |
| Qy    | 134 -----TESGKE--ENTIQQPKV-----KESTTS 156                                                                          |
| Db    | 1803 LFAVNOKNMATEKKERAVESGKRQENTLKGENDILDEANLRADEINSIDYDVLIQTK 1862                                                |
| Qy    | 157 OPSGYNTIDENISN---QPELNLPINEYENKARPLSTMSA---QESTKRVNQL 206                                                      |
| Db    | 1863 LPPMSEELNDKIDDQSIEKURKLAEVSKQESHAQNLNDSSAVLDGILDEBAKNISNAT 1922                                               |
| Qy    | 207 AAEQG-SNVNHLIKVTDQSDITEGYDSEGVIKAHDENLYDVTFEVVDKVKSGDMTV 265                                                   |
| Db    | 1923 AAFKAYSNIKYI-----DEAKVAK--EAKDAHEAT----KLATGPR---G 1961                                                       |
| Qy    | 266 IDKNTWPSDLTDSFTI-----PKIDNSGEIATGT---YDNKQKQITYTFD 313                                                         |
| Db    | 1962 LIKEDAKGCLQSKVLPDKRTRIENA DARRNGDLRTLTNDLG 2021                                                               |
| Qy    | 314 KYENT-----KAHLKLTSYTDKSVPNNTR-----LDVEYKTAASSVNTIT 356                                                         |
| Db    | 2022 KLSAIPNDTAALKQAVDKAROANDPKVLAQITELHQNDLGKKNYKLADSAVTKNA 2081                                                  |
| Qy    | 357 VEYORPENR-TANLQSMFTND-----TKHNFVEOTIYINFLRY 396                                                                |
| Db    | 2082 V-VKDPSPNKITADADTVKNIQEADRLIDKLKPKELEDNLKKNISEKEILINQARKQ 2140                                                |
| Qy    | 397 AKETNNISGND-----EGS-----TIIIDSPSIKV-----YK 425                                                                 |

RESULT 11  
 YBL047C\_YAST STANDARD; PRT; 1381 AA.  
 P24216; 01-FEB-1994 (Rel. 28, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DR 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 150.8 kDa protein in SGD-OCRI intergenic region.  
 GN YBL047C OR YBL0520 OR YBL0501.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes;  
 NCBI\_TaxId:4932;  
 RN [1]  
 RP SEQUENCE OF 1-961 FROM N.A.  
 RC STRAIN=S28C;  
 RX MEDLINE=9516707; PubMed=7871888;  
 RA de Wergifosse P., Jacques B., Jonniaux J.-L., Purnelle B., Skala J.,  
 RT "The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome II reveals homologues to bacterial proline synthetase and murine alpha-adaptin, as well as a new permease and a DNA-binding protein.";  
 RL Yeast 10:1489-1496(1994).  
 [2]  
 RN SEQUENCE OF 579-1381 FROM N.A.  
 RC STRAIN=S28C;  
 RX MEDLINE=94205266; PubMed=8154187;  
 RA Scherens B., el Bakoury M., Vierendeels F., Dubois E., Messenquy F.,  
 RT "Sequencing and functional analysis of a 32,560 bp segment on the left arm of yeast chromosome II. Identification of 26 open reading frames, including the KIP1 and SEC17 genes.";  
 RL Yeast 9:1355-1371(1993).  
 -- SIMILARITY: BELONGS TO THE VDP/US01/YBL047C FAMILY.  
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RESULT 12  
 YBL047C\_YAST STANDARD; PRT; 1165 AA.  
 P235808; 01-OCT-1996 (Rel. 34, Last sequence update)  
 AC P53950; 01-OCT-1996 (Rel. 34, Created)  
 DR 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE Hypothetical 128.1 kDa protein in OMP2-MSC3 intergenic region.  
 GN YNL054W OR N2467 OR YNL2467W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 NCBI\_TaxId:4932;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S28C / FV1676;  
 RX MEDLINE=96021608; PubMed=8533472;  
 RA Bergez P., Doignon F., Crouzet M.;



|                    |                                                                                                                                                                  |                                                             |                              |
|--------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|------------------------------|
| QY                 | 190                                                                                                                                                              | STTSQAQSI-----KRVTNOLAEQGSNVNHLIKYDQI---TEGY-----           | 229                          |
| DR                 | KW                                                                                                                                                               | SGD: s0005428; YGR16C.                                      |                              |
| Db                 | 1120                                                                                                                                                             | HHAQQRSVDETTIDEKLERTIDNELAT--VDVNBSLAAKNEQVQDLFTDEYAVDDN    | 1176                         |
| SEQUENCE           | 817 AA;                                                                                                                                                          | 90797 MW;                                                   | E52C5D659d63BEBB CRC64;      |
| QY                 | 230                                                                                                                                                              | --DDSGVVIKAH---DAENLYDITFE-----VDDKVKGSDTMTWDI              | 266                          |
| DR                 | Best Local Similarity                                                                                                                                            | 21.0%                                                       | Score 184; DB 1; Length 817; |
| Db                 | 1177                                                                                                                                                             | GMQDDSGGQYQIKEDLFVGDNNIEKTEIQTSSLNQBCERVNDVBDI-SGEAKNESS    | 1235                         |
| QY                 | 267                                                                                                                                                              | DKNTVP-----SDIIDS---FTPKIKDNSEGTATGTYDKNKQITYP              | 308                          |
| Db                 | 1236                                                                                                                                                             | EMIQVYDVLPEAKVTGDBQISPLQDEKINLETMDTKDNDQI---CLEKEN-         | 1285                         |
| QY                 | 351                                                                                                                                                              | -----"INKTIVVEQRPNRNTANLQSMFTNDTAKHIVETQTYIINPLRYAKETN      | 404                          |
| DR                 | ESTEEQYQETTIPF-KPDESKM-----ENSESEVSVDOSBISLN---SHKSEEFFI                                                                                                         | 1393                                                        |                              |
| QY                 | 309                                                                                                                                                              | TDVYDKYENIK-----AHLKTSVYDKSKVP---NNNTKL---DVEYKTA           | 350                          |
| Db                 | 1286                                                                                                                                                             | TEYIEVTDSPQFATDLSDHAGRELT--VDQNSANLQFCENPTKTLIAHHIEYEVADSD  | 1343                         |
| QY                 | 1344                                                                                                                                                             | -----"INKTIVVEQRPNRNTANLQSMFTNDTAKHIVETQTYIINPLRYAKETN      | 404                          |
| DR                 | ESTEEQYQETTIPF-KPDESKM-----ENSESEVSVDOSBISLN---SHKSEEFFI                                                                                                         | 1393                                                        |                              |
| QY                 | 405                                                                                                                                                              | SONGDEGSTIIDSTIKVKGDNQNPDSNRIVY-SEYEDVTN--DDYAQLGNNND       | 461                          |
| Db                 | 1394                                                                                                                                                             | S-----KDYQL-EQCLPDVPLPNLDEDDEFULTEQDVHHEHQNNDS              | 1435                         |
| QY                 | 462                                                                                                                                                              | NINFGNIDSPPYIIVKSYDPNPKDYYTIIQTVTMQTTNEYT-GEFRASYNTIA       | 520                          |
| Db                 | 1436                                                                                                                                                             | GA-----STFITSV---DEDKERERRESVSKDEESEEEFGDVLSSVDKTSQEV       | 1483                         |
| QY                 | 521                                                                                                                                                              | SSGQGQDLPPEKTYKGDYVWEDVKGQIWND-NERKPLSVL-----               | 564                          |
| Db                 | 1484                                                                                                                                                             | LSGLAQ---EPSY-LGD--NEESEDMENAEITLNENPSNDIVDFMVSQMTETKIIA    | 1534                         |
| QY                 | 565                                                                                                                                                              | -----VLTYPDGTSK--SVRTDEGKQFD 588                            |                              |
| Db                 | 1535                                                                                                                                                             | EVQEIQETVTFQDPAKLNKLENARKEKTYVE 1569                        |                              |
| RESULT             | 14                                                                                                                                                               |                                                             |                              |
| YG4A_YEAST         |                                                                                                                                                                  | STANDARD;                                                   | PRT; 817 AA.                 |
| ID                 |                                                                                                                                                                  |                                                             |                              |
| AC                 | P46949;                                                                                                                                                          |                                                             |                              |
| DT                 | 01-NOV-1995 (Rel. 32, Created)                                                                                                                                   |                                                             |                              |
| DT                 | 01-NOV-1995 (Rel. 32, Last sequence update)                                                                                                                      |                                                             |                              |
| DT                 | 01-NOV-1997 (Rel. 35, Last annotation update)                                                                                                                    |                                                             |                              |
| DE                 | Hypothetical 90.8 kDa protein in RRP41-SNG1 intergenic region.<br>YGR196C OR G7589.                                                                              |                                                             |                              |
| QY                 | 382                                                                                                                                                              | HTVEOPTIYINPLRYASAKETNYNISNGDEGSTIIDSTIKVKGDNQNPDSNRIVY     | 441                          |
| Db                 | 478                                                                                                                                                              | DSALQPQNQDITI---ENTLNLSNSGLELNSGSDDEDHINEDKVLEESSVKDSTDVDSW | 533                          |
| QY                 | 442                                                                                                                                                              | SEYEDVTNDDPAQLGNNNDVNINFGNIDSP--YII-----                    |                              |
| Db                 | 534                                                                                                                                                              | KPDSEALRSGFVQ-----DTANKKAPPYVIDSNGKLVLDTPASMKVPRVSTY        | 584                          |
| QY                 | 482                                                                                                                                                              | -----PNK---DDYTIIQTVTMQTTNEYTGEFRASYNTIA                    |                              |
| Db                 | 585                                                                                                                                                              | STSSGQDVKAPKPKVANEKMTSDNGYRNFND                             |                              |
| QY                 | 531                                                                                                                                                              | P---EKTYKTGDYVWEDVKGQIWNDNERKPLSVL 564                      |                              |
| Db                 | 630                                                                                                                                                              | PLPMPDQEQLMAGN-----DNSTIDNDNNNTANDL 660                     |                              |
| SEQUENCE FROM N.A. |                                                                                                                                                                  |                                                             |                              |
| RC                 | STRAIN=S288C;                                                                                                                                                    |                                                             |                              |
| RX                 | MEDLINE=960766533; PubMed=7502584;                                                                                                                               |                                                             |                              |
| RA                 | Guerreiro P., Maia e Silva T., Arroyo J.,                                                                                                                        |                                                             |                              |
| RA                 | Garcia-Gonzalez M., Garcia-Saez M.I., Rodrigues-Pousada C.,                                                                                                      |                                                             |                              |
| RA                 | Nombela C.;                                                                                                                                                      |                                                             |                              |
| RT                 | "The complete sequence of a 9000 bp fragment of the right arm of Saccharomyces cerevisiae chromosome VII contains four previously unknown open reading frames."; |                                                             |                              |
| RT                 | yeast 11:1087-1091(1995).                                                                                                                                        |                                                             |                              |
| RL                 |                                                                                                                                                                  |                                                             |                              |
| RESULT             | 15                                                                                                                                                               |                                                             |                              |
| RBP2_PLAVB         |                                                                                                                                                                  | STANDARD;                                                   | PRT; 1251 AA.                |
| ID                 | RBP2_PLAVB                                                                                                                                                       |                                                             |                              |
| AC                 | 000799;                                                                                                                                                          |                                                             |                              |
| DT                 | 01-APR-1993 (Rel. 25, Created)                                                                                                                                   |                                                             |                              |
| DT                 | 01-APR-1993 (Rel. 25, Last sequence update)                                                                                                                      |                                                             |                              |
| DT                 | 01-OCT-1995 (Rel. 34, Last annotation update)                                                                                                                    |                                                             |                              |
| DE                 | Reticulocyte binding protein 2 (Fragment).                                                                                                                       |                                                             |                              |
| GN                 | RBP2.                                                                                                                                                            |                                                             |                              |
| SEQUENCE FROM N.A. |                                                                                                                                                                  |                                                             |                              |
| OS                 | Plasmidium vivax (strain Belem').                                                                                                                                |                                                             |                              |
| OX                 | Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.                                                                                                     |                                                             |                              |
| OC                 | NCBI_TAXID=31273;                                                                                                                                                |                                                             |                              |
| RT                 | "A reticulocyte binding protein complex of Plasmodium vivax merozoites";                                                                                         |                                                             |                              |
| RT                 | Cell 69:1213-1226(1992).                                                                                                                                         |                                                             |                              |
| RL                 |                                                                                                                                                                  |                                                             |                              |

Search completed: July 30, 2002, 10:41:04  
Job time: 548 sec

TUE JUL 30 11:46:41 2002

us-09-147-405-11.rsp

GenCore version 4.5  
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OM protein - protein search, using sw model

Run On: July 30, 2002, 10:31:01 ; Search time 88.07 Seconds  
(without alignments)  
1164.823 Million cell updates/sec

Title: Perfect score!  
Sequence: US-09-147-405-11  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTRMBL19:  
1: sp\_archea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phage:  
10: sp\_plant:  
11: sp Rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_rvirus:  
16: sp\_bacteriapl:  
17: sp\_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

| Result No. | Score  | Query | Match Length | DB ID  | Description |
|------------|--------|-------|--------------|--------|-------------|
| 1          | 3015   | 97.7  | 1092         | 2      | 070022      |
| 2          | 2812.5 | 91.1  | 931          | 2      | 09K113      |
| 3          | 1812.5 | 37.7  | 1171         | 2      | 09KWX6      |
| 4          | 1146.5 | 37.1  | 1166         | 2      | 086489      |
| 5          | 1139.5 | 36.9  | 1141         | 16     | 099W6       |
| 6          | 1139.5 | 36.9  | 1141         | 16     | 093F7       |
| 7          | 576    | 18.7  | 1315         | 2      | 086488      |
| 8          | 559    | 18.1  | 1385         | 16     | 099W7       |
| 9          | 506    | 16.4  | 1733         | 2      | 09K114      |
| 10         | 490    | 15.9  | 953          | 16     | 099W48      |
| 11         | 460.5  | 14.9  | 881          | 2      | 093MH7      |
| 12         | 455    | 14.8  | 2            | 086487 |             |
| 13         | 452    | 14.6  | 933          | 2      | Q53653      |
| 14         | 452    | 14.6  | 16           | Q932C5 |             |
| 15         | 452    | 14.6  | 989          | 16     | Q99V4       |
| 16         | 405.5  | 13.1  | 877          | 16     | Q99R07      |

RESULTS

| RESULT ID                                                                       | 1                                                                                                                                                                             | PRELIMINARY;                                       | PRT; 1092 AA. |
|---------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------|---------------|
| 070022                                                                          | 070022;                                                                                                                                                                       |                                                    |               |
| AC                                                                              | DT                                                                                                                                                                            | 01-AUG-1998 (TREMBLER. 07, Created)                |               |
|                                                                                 | DT                                                                                                                                                                            | 01-AUG-1998 (TREMBLER. 07, Last sequence update)   |               |
|                                                                                 | DT                                                                                                                                                                            | 01-JUN-2001 (TREMBLER. 17, Last annotation update) |               |
| OS                                                                              | DE                                                                                                                                                                            | FIBRINOGEN BINDING PROTEIN PRECURSOR.              |               |
| Bacteria; Firmicutes; Bacillus/Staphylococcus group; Staphylococcus epidermidis | OS                                                                                                                                                                            |                                                    |               |
| Bacillus; Firmicutes; Bacillus/Staphylococcus group; Staphylococcus epidermidis | OC                                                                                                                                                                            |                                                    |               |
| Bacillus/Staphylococcus group; Staphylococcus                                   | OC                                                                                                                                                                            |                                                    |               |
| NCBI_TaxID-1282; [1]                                                            | OX                                                                                                                                                                            |                                                    |               |
| [1]                                                                             | RN                                                                                                                                                                            |                                                    |               |
| SEQUENCE FROM N.A.                                                              | RP                                                                                                                                                                            |                                                    |               |
| RC                                                                              | RC                                                                                                                                                                            |                                                    |               |
| RX                                                                              | RX                                                                                                                                                                            |                                                    |               |
| RA                                                                              | RA                                                                                                                                                                            |                                                    |               |
| RT                                                                              | "A Fibrinogen-binding protein of <i>Staphylococcus epidermidis</i> ."; Nilsson M., Frykberg L., Flock J.I., Peil L., Lindberg M., Guss B.; Infect. Immun. 66:2666-2673(1998). |                                                    |               |
| RL                                                                              | RL                                                                                                                                                                            |                                                    |               |
| DR                                                                              | DR                                                                                                                                                                            |                                                    |               |
| InterPro; IPR01899; Gram_pos_anchor.                                            | IPR01899                                                                                                                                                                      |                                                    |               |
| DR                                                                              | DR                                                                                                                                                                            |                                                    |               |
| InterPro; IPR01899; Gram_pos_anchor; 1.                                         | IPR01899                                                                                                                                                                      |                                                    |               |
| DR                                                                              | DR                                                                                                                                                                            |                                                    |               |
| PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.                                | PS00343                                                                                                                                                                       |                                                    |               |
| DR                                                                              | DR                                                                                                                                                                            |                                                    |               |
| KW                                                                              | KW                                                                                                                                                                            |                                                    |               |
| FT                                                                              | FT                                                                                                                                                                            |                                                    |               |
| FT                                                                              | FT                                                                                                                                                                            |                                                    |               |
| FT                                                                              | FT                                                                                                                                                                            |                                                    |               |
| SEQUENCE                                                                        | SEQUENCE                                                                                                                                                                      |                                                    |               |
| 093F7 staphylococ                                                               | 093F7 staphylococ                                                                                                                                                             |                                                    |               |
| 086488 staphylococ                                                              | 086488 staphylococ                                                                                                                                                            |                                                    |               |
| 099W47 staphylococ                                                              | 099W47 staphylococ                                                                                                                                                            |                                                    |               |
| 099W7 staphylococ                                                               | 099W7 staphylococ                                                                                                                                                             |                                                    |               |
| Q53653 staphylococ                                                              | Q53653 staphylococ                                                                                                                                                            |                                                    |               |
| Q932C5 staphylococ                                                              | Q932C5 staphylococ                                                                                                                                                            |                                                    |               |
| Q99V4 staphylococ                                                               | Q99V4 staphylococ                                                                                                                                                             |                                                    |               |
| Q99R07 staphylococ                                                              | Q99R07 staphylococ                                                                                                                                                            |                                                    |               |

Query Match 97.7%; Score 3015; DB 2; Length 1092;  
Best Local Similarity 99.7%; Pred. No. 6.28-113;  
Matches 582; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSDEEKNDVINVNNQSNIDDDNNQIKKEETNNQDIERSEDRDTEESTPNDENATEFQK 67  
Db 75 SSDEEKNDVINVNNQSNIDDDNNQIKKEETNNQDIERSEDRDTEESTPNDENATEFQK 134

QY 68 TQDQNTLTHEEVEKREKSVESVSSNSIDAQQPHTTIREBESVTQSDVNEYDSHDFANS 127



| Db                    | QY                                                                                                                                                                                                                         | 66 ARTSDNRKEVSEENNSTENNTPNPIKE-INTDSPEAKESTSSSTQKQONINVAT 123 |
|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------|
| QY                    | 66 OKPQDNLHLETEREVKES--SSVSESSNSIDTAQPSHTTIRESEVOTSNDYEDSHVS 122                                                                                                                                                           | QY                                                            |
| Db                    | 124 TEKPON--IEKENVKPSTDKTADETSVILEEKKAPNT--NNDTTKPS----TS 172                                                                                                                                                              | Db                                                            |
| QY                    | 123 DFANSKIKESNT--ESEKEENTIEQPNVKVEESTSOPSGYINIDEKIS-NQDELLNP 178                                                                                                                                                          | QY                                                            |
| Db                    | 173 EPSTSEQTPTKPTPOESTNIENSOPQTPSKVD--NOVTDATNPCKPVNUKSEBLKNPP 229                                                                                                                                                         | Db                                                            |
| QY                    | 179 -----INEVENKARPLISTSAQPSIKR-----TQNLAQEQSNVNHILKVTDQ 223                                                                                                                                                               | QY                                                            |
| Db                    | 230 EKLUKLVRNSNDHSDTRPVATAPTSVAPKRVNAMRFAQPAVASNNVNDLKVTQ 289                                                                                                                                                              | Db                                                            |
| QY                    | 224 STREGYDSEGVTKAHDAENLIVTYDVEUDKVKSGDTMVUDIDKNTVDSLADSPFTPK 283                                                                                                                                                          | QY                                                            |
| Db                    | 290 TIKVG-DGKDNNVAADHGKDIETDTEFTIDNKVYKKGDTWINTDKNVIPSDLTDKNDPID 348                                                                                                                                                       | Db                                                            |
| QY                    | 340 LDVEYKTALSVNKNTTVEYORPENRNTANLQSMFTNTDKNHTVEQTINYINPLYSAKE 399                                                                                                                                                         | QY                                                            |
| Db                    | 399 LNLTTFATDADKETSKNVKVEQKPKIVKDESNIQSIFSHLDITKHEVETQVNPPLKLNAKI 458                                                                                                                                                      | Db                                                            |
| QY                    | 400 TNNI-----SGND---EGSTIDDSIIKVVKVGDNQNLPSNRIVYSEVEDTNQ 450                                                                                                                                                               | QY                                                            |
| Db                    | 459 TNYTAKTISKSGVADNGDYINGGSTIDSNTDNEBIVKVKVQASQOLPNSKIXYQSYEDNTN 518                                                                                                                                                      | Db                                                            |
| QY                    | 451 DYQLGNN-----NDUNVINFQMDSPVIKVKYDNNKDDTTIQTUTMOTINETGEF 507                                                                                                                                                             | QY                                                            |
| Db                    | 519 ----VINKVNGTNMANINFQCDIDSSYIVKVKVQGAFLAVQGQVRMT----TNKY 571                                                                                                                                                            | Db                                                            |
| QY                    | 508 RTASYDN-----TIASTSSQGQGQLPPEKTYKIDYVWEDVDKQCIQNTNDNEK 558                                                                                                                                                              | QY                                                            |
| Db                    | 572 NISSYAGTITLFQQLTLYVTVSVK----PEEKLYKIGDYVWEDVDKVQVQGQDSKER 626                                                                                                                                                          | Db                                                            |
| QY                    | 559 PLSHVLYLTYDPTSKYTFDPEQKQFGVQ 591                                                                                                                                                                                       | QY                                                            |
| Db                    | 627 PMANVLYLTYDPTGKSTRTDANGHYERGLK 659                                                                                                                                                                                     | Db                                                            |
| RESULT                | 4                                                                                                                                                                                                                          |                                                               |
| ID                    | 086489 PRELIMINARY; PRT; 1166 AA.                                                                                                                                                                                          |                                                               |
| AC                    | 086489; 01-NOV-1998 (TREMBLrel. 08, last sequence update)                                                                                                                                                                  |                                                               |
| DT                    | 01-NOV-1998 (TREMBLrel. 08, last annotation update)                                                                                                                                                                        |                                                               |
| DE                    | SDR_E PROTEIN.                                                                                                                                                                                                             |                                                               |
| GN                    | SDR_E.                                                                                                                                                                                                                     |                                                               |
| OS                    | Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus aureus.                                                                                                                                          |                                                               |
| OS                    | Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus aureus.                                                                                                                    |                                                               |
| RN                    | [1]                                                                                                                                                                                                                        |                                                               |
| RP                    | SEQUENCE FROM N.A.                                                                                                                                                                                                         |                                                               |
| RC                    | STRAIN=NEWMAN;                                                                                                                                                                                                             |                                                               |
| RC                    | MEDLINE-99098700; PubMed=9884231;                                                                                                                                                                                          |                                                               |
| RA                    | Josephson E., McCrea K., Ni Edhin D., O'Connell D., Cox J., Hook M., Foster T.J.; "Three new members of the serine-aspartate repeat protein multigene family of Staphylococcus aureus.", Microbiology 144:3387-3395(1998). |                                                               |
| RL                    | EMBL: AJ005647; CA006652; 1; -.                                                                                                                                                                                            |                                                               |
| DR                    | InterPro: IPR001899; Gram_pos_anchor; I.                                                                                                                                                                                   |                                                               |
| DR                    | PROSITE: PS0043; GRAM_POS_ANCHORING; UNKNOWN_1.                                                                                                                                                                            |                                                               |
| SQ                    | SEQUENCE: 1166 AA; 126548 MW; 750A7B0135287D4A CRC64;                                                                                                                                                                      |                                                               |
| Query Match           | 37.1%; Score 1146.5; DB 2; Length 1166;                                                                                                                                                                                    |                                                               |
| Best Local Similarity | 42.3%; Pred. No. 1; ge-38;                                                                                                                                                                                                 |                                                               |
| Matches               | 263; Conservative 110; Mismatches 191; Indels 55; Gaps 18;                                                                                                                                                                 |                                                               |
| QY                    | 8 SSDEEKNDVNNQSQSTDNNQI--IKKEETNNYQIEKISEDRAFTNTDNEATFL 65                                                                                                                                                                 |                                                               |

|          |                                                                     |          |                                                                                                                                    |
|----------|---------------------------------------------------------------------|----------|------------------------------------------------------------------------------------------------------------------------------------|
| DR       | Pfam: PF00746; Gram_pos_anchor; 1.                                  | RA       | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,                                                                       |
| DR       | PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.                    | RA       | Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |
| KW       | Complete proteome.                                                  | RA       | Mizutani-Uji Y., Takahashi N.K., Swano T., Inoue R.-I., Kaito C.,                                                                  |
| SEQUENCE | 1141 AA; 124026 MW; 445419D0B8C5A4F8 CRC64;                         | RA       | Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J., Kanemitsu K., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., |
| QY       | 8 SSPEEKNDVNNNOSINTDDNNQIKKEETNNYDGIEKRSERDFESTINDENERATFLOK 67     | RA       | Hattori M., Osasawara N., Hayashi H., Hiramatsu K.,                                                                                |
| Db       | 69 SDNKEVSETENNNTENDSTNP1-KKETNT-DSPEAKEESTSSTQQQQNNVATTE 125       | RT       | "Whole genome sequencing of meticillin-resistant <i>Staphylococcus</i> aureus.",                                                   |
| Qy       | 68 TPQDNTHLBEVEKES--SSVESSNSIDTAQPSHTTINREESVOTSDNVEDSHVSDF 124     | RT       | Lancet, 357:1225-1240 (2001);                                                                                                      |
| Db       | 126 TKPON-IEKENVKSTDKTATEDTSVILEKKAPNT-NNDVTKPS----- 170            | RL       | DRB; AP003359; BA56725.1; -.                                                                                                       |
| Qy       | 179 -----INYEENKARPLST-TSAPQ---SIKRVTVNOLAEGSGSNVNLHILKVDQSI 225    | KW       | Complete proteome.                                                                                                                 |
| Db       | 227 LKELYRNDNNITDRSTKPVATAPSVAKRNLANKMRPAVAAVASNNYNDLITVKTQI 286    | SEQUENCE | 1141 AA; 124038 MW; E679F/C2991846D9 CRC64;                                                                                        |
| Qy       | 226 TEGYDSEGVKTDKATQOYTFTDVKTDIKRKLTLYSIDKQAVP-NETSNLFTA 285        | QY       | 8 SSPEEKNDVNNNOSINTDDNNQIKKEETNNYDGIEKRSERDFESTINDENERATFLOK 67                                                                    |
| Db       | 287 KVQ-DCKDNVAAHOCKDIEYDTEFTIDNKVKKGDTMTINYDKNVIPSDLTDKNDPDT 345   | QY       | Best Local Similarity 36.1%; Pred. No. 3.6e-38; Matches 266; Conservative 99; Mismatches 193; Indels 59; Gaps 19;                  |
| Qy       | 286 DNSGETIATGTYDNKNQKQIYTFTDVKDYENKAHLKLTSYIDKSKVNNNTKLDEVK 345    | Db       | 69 SDNKEVSETENNNTENDSTNP1-KKETNT-DSPEAKEESTSSTQQQQNNVATTE 125                                                                      |
| Db       | 346 DPSGEVIAGKTFDKATQOYTFTDVKTDIKRKLTLYSIDKQAVP-NETSNLFTA 404       | Qy       | 68 TPQDNTHLBEVEKES--SSVESSNSIDTAQPSHTTINREESVOTSDNVEDSHVSDF 124                                                                    |
| Qy       | 346 TALSSVNKTIVVEYDPRNENRNTANQSMFTNIDTKNHTVQTYINPLR/SAKENVNIS 405   | Qy       | 179 -----INYEENKARPLST-TSAPQ---SIKRVTVNOLAEGSGSNVNLHILKVDQSI 225                                                                   |
| Db       | 405 TAGKETSONSVSDQPMWGDNSNIQSIFKLDENKQTQFQOQVYVPLKTTATVKTQI 464     | Db       | 126 TKPON-IEKENVKSTDKTATEDTSVILEKKAPNT-NNDVTKPS----- 170                                                                           |
| Qy       | 406 GNG-----DEGSTIIDSTIKVVKYQDNQLPDSRIVDSEYEDVTD-DYAQI 455          | Qy       | 125 ANSKTKESTNT-DSSGEKEETIEOPNKVKESTNT-QPSG3YTNIDEKIS-NODELLNLP-- 178                                                              |
| Db       | 465 GSQVDDYGNKLQKNGSTIDONTEIKVVKYQPNQOLPQSNRRIYDPSQYEDVTSQFDNKK 524 | Db       | 171 -TSEIQTKPTQESTNINIENSQOPTPSKVD--NOVTDATNPKEPVNYSKEELKNPEK 226                                                                  |
| Qy       | 456 GNNNDVNINFQNDSPYIPIKVSKDPNQKDDYTTIQTQVTMQTTNEYTGFRASYDT 515     | Qy       | 226 TEGYDSEGVKTDKATQOYTFTDVKTDIKRKLTLYSIDKQAVP-NETSNLFTA 404                                                                       |
| Db       | 525 FSNNYATLDFGDIINSAYIKVVKSKYPTSDGELDIAQGTSMRTT-DKY-GYNYAGSNF 582  | Db       | 287 KVQ-DCKDNVAAHOCKDIEYDTEFTIDNKVKKGDTMTINYDKNVIPSDLTDKNDPDT 345                                                                  |
| Qy       | 516 IAFSTSSGGOGSDL-PPEKTYKIGDQVWEDVKDGQTQNTDNEKPLSNVNLVLTYPDGTS 574 | Qy       | 286 DNSGETIATGTYDNKNQKQIYTFTDVKDYENKAHLKLTSYIDKSKVNNNTKLDEVK 345                                                                   |
| Db       | 583 IVTSNDTGGDGTVKPEEKLYKIGDQVWEDVKDGQVGTDSKEKPMANVNLVLTYPDGTT 642  | Db       | 405 TAGKETSONSVSDQPMWGDNSNIQSIFKLDENKQTQFQOQVYVPLKTTATVKTQI 464                                                                    |
| Qy       | 575 KSVRTDEGKQFDGQ 591                                              | Qy       | 406 GNG-----DEGSTIIDSTIKVVKYQDNQLPDSRIVDSEYEDVTD-DYAQI 455                                                                         |
| Db       | 643 KSVRTDANGHYEFGGLK 659                                           | Db       | 465 GSQVDDYGNKLQKNGSTIDONTEIKVVKYQPNQOLPQSNRRIYDPSQYEDVTSQFDNKK 524                                                                |
| RESULT   | 6                                                                   | Qy       | 456 GNNNDVNINFQNDSPYIPIKVSKDPNQKDDYTTIQTQVTMQTTNEYTGFRASYDT 515                                                                    |
| 0932F7   | PRELIMINARY; PRT: 1141 AA.                                          | Db       | 525 FSNNYATLDFGDIINSAYIKVVKSKYPTSDGELDIAQGTSMRTT-DKY-GYNYAGSNF 582                                                                 |
| ID       | 0932F7;                                                             | Qy       | 516 IAFSTSSGGOGSDL-PPEKTYKIGDQVWEDVKDGQTQNTDNEKPLSNVNLVLTYPDGTS 574                                                                |
| AC       | 0932F7;                                                             | Db       | 583 IVTSNDTGGDGTVKPEEKLYKIGDQVWEDVKDGQVGTDSKEKPMANVNLVLTYPDGTT 642                                                                 |
| DT       | 01-DEC-2001 (TREMBLrel. 19, last sequence update)                   | Qy       | 575 KSVRTDEGKQFDGQ 591                                                                                                             |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                 | Db       | 643 KSVRTDANGHYEFGGLK 659                                                                                                          |
| DE       | SER-ASP RICH FIBRINOGEN-BINDING PROTEIN.                            | QY       | 516 IAFSTSSGGOGSDL-PPEKTYKIGDQVWEDVKDGQTQNTDNEKPLSNVNLVLTYPDGTS 574                                                                |
| DN       | SDRE OR SAV0563.                                                    | Db       | 583 IVTSNDTGGDGTVKPEEKLYKIGDQVWEDVKDGQVGTDSKEKPMANVNLVLTYPDGTT 642                                                                 |
| OS       | Staphylococcus aureus (strain Mu50).                                | QY       | 575 KSVRTDEGKQFDGQ 591                                                                                                             |
| OC       | Bacteria; Firmicutes; Bacillus/Clostridium group;                   | Db       | 643 KSVRTDANGHYEFGGLK 659                                                                                                          |
| OC       | Bacillus/Staphylococcus group; Staphylococcus.                      | QY       | 516 IAFSTSSGGOGSDL-PPEKTYKIGDQVWEDVKDGQTQNTDNEKPLSNVNLVLTYPDGTS 574                                                                |
| RN       | [1]                                                                 | Db       | 583 IVTSNDTGGDGTVKPEEKLYKIGDQVWEDVKDGQVGTDSKEKPMANVNLVLTYPDGTT 642                                                                 |
| RP       | SEQUENCE FROM N.A.                                                  | QY       | 575 KSVRTDEGKQFDGQ 591                                                                                                             |
| RX       | MEDLINE-21311952; PubMed-11418146;                                  | Db       | 643 KSVRTDANGHYEFGGLK 659                                                                                                          |
| RA       | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  | OS       | Staphylococcus aureus.                                                                                                             |

|                       |                                                                       |                       |                                                                                                                                                                                                                                                                                                                         |
|-----------------------|-----------------------------------------------------------------------|-----------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OC                    | Bacteria; Firmicutes; Bacillus/Clostridium group;                     | DT                    | 01-DEC-2001 (TREMBREL. 19, last annotation update)                                                                                                                                                                                                                                                                      |
| OC                    | Bacillus/staphylococcus group; Staphylococcus.                        | DE                    | SER-ESP RICH FIBRINOGEN-BINDING, BONE SIALOPROTEIN-BINDING                                                                                                                                                                                                                                                              |
| OX                    |                                                                       | DE                    | PROTEIN.                                                                                                                                                                                                                                                                                                                |
| RN                    | [1]                                                                   | GN                    | SDRD OR SAV0562.                                                                                                                                                                                                                                                                                                        |
| RP                    | SEQUENCE FROM N.A.                                                    | OS                    | Staphylococcus aureus (strain Mu50).                                                                                                                                                                                                                                                                                    |
| RC                    | STRAIN-NEWMAN;                                                        | OS                    | Staphylococcus aureus (strain Mu50).                                                                                                                                                                                                                                                                                    |
| RX                    | MEDLINE=99098700; PubMed=9884231;                                     | RA                    | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                                                                                                                                                                                                       |
| RA                    | Jossersson E., McCrea K., Ni Edhin D., O'Connell D., Cox J., Hock M., | RA                    | Bacillus/staphylococcus group; Staphylococcus.                                                                                                                                                                                                                                                                          |
| RA                    | Foster T.J.;                                                          | RT                    | "Three new members of the serine-aspartate repeat protein multigene family of Staphylococcus aureus.";                                                                                                                                                                                                                  |
| RT                    | Microbiology 144:3387-3395 (1998).                                    | RL                    | Microbiology 144:3387-3395 (1998).                                                                                                                                                                                                                                                                                      |
| DR                    | EMBL; AJ005646; CAA6651.1; -.                                         | DR                    | InterPro: IPR01899; Gram-pos_anchor.                                                                                                                                                                                                                                                                                    |
| DR                    | Pfam; PF00746; Gram_pos_anchor; 1.                                    | DR                    | PFam; PF00746; Gram_pos_anchor; 1.                                                                                                                                                                                                                                                                                      |
| SEQUENCE              | 1315 AA; 142775 MW; 58D4E1F48EE6A689 CRC64;                           | SO                    | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                      |
| Query Match           | 18.7%; Score 576; DB 2; Length 1315;                                  | RC                    | SPECIES=S. aureus (strain N315) and S.aureus (strain Mu50);                                                                                                                                                                                                                                                             |
| Best Local Similarity | 30.1%; Pred. No. 1. 2e-15;                                            | RX                    | MEDLINE=2311952; PubMed=11418146;                                                                                                                                                                                                                                                                                       |
| Matches               | 186; Conservative 112; Mismatches 228; Indels 92; Gaps 29;            | RA                    | Kuroda M., Ohta T., Uchihara Y., Baba T., Yuzawa H., Kobayashi I.,                                                                                                                                                                                                                                                      |
| ..                    | ..                                                                    | RA                    | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsunaru H., Matuyama A., Murakami H., Hosoya A., Mizuani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C., Sekimizu K., Hirakawa H., Kuhara S., Yabuzaki J., Shiba T., Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., |
| 8                     | SSDEEKNDV--INNNQSINTDDNNQIKEETNNYDGIEKRSEURTESTNTVDE-NEAT             | RA                    | Hattori M., Ogasawara N., Hayashi H., Hirayama S., Hosoya A.,                                                                                                                                                                                                                                                           |
| Db                    | 55 STNKELNEATNTSASDNQSSDKVDMQOLNOEDNTKNDQNKEVNNSCGNETTSNGNKLIEKE      | RA                    | "Whole genome sequencing N of meticillin-resistant Staphylococcus aureus.";                                                                                                                                                                                                                                             |
| QY                    | 64 FLQKIPQDNTLHLEEVEKESSESVESSNSSIDTAQQPSHTTINREVSQVTSDNVEDSHVSD      | RT                    | aureus.;                                                                                                                                                                                                                                                                                                                |
| Db                    | 115 SYVOSTGKVKEVSTAKSDEASPKNPSENEDNTQ--TISNQALQ-PDLLENKVNN 168        | RL                    | Lancet 357:1225-1240(2001).                                                                                                                                                                                                                                                                                             |
| QY                    | 124 FANSKIKESNTESKGKENTIEQPNKVKESTDTSQPSGYNT-DEKT-SNQELL--NLPIN 180   | DR                    | EMBL; AP00313; BAB1751; -.                                                                                                                                                                                                                                                                                              |
| Db                    | 169 ---VQPTNEENKKD-----AKTEST-----LANKSDAIKSNETLIVNNNS 209            | DR                    | EMBL; AP003359; BAB56724; -.                                                                                                                                                                                                                                                                                            |
| QY                    | 181 EYENKARPLSLTSQAOP---SIKYTVNOLAAEGSNSVNHILKVKVMDQISITEGYDSEGVI     | RA                    | InterPro: IPR01899; Gram_pos_anchor.                                                                                                                                                                                                                                                                                    |
| Db                    | 210 NNENNADILPKSTAPKRNTRMRMIAVQESPSTEAKNVNDLITSNNTLVVDAKNNKIV         | RA                    | Pfam; PF00746; Gram_pos_anchor; 1.                                                                                                                                                                                                                                                                                      |
| QY                    | 237 KAHDARNLIVYTFEDVKYSGDPMWIDKNTV-----PSDLDSFTIPKID-NSG 289          | RT                    | Complete proteome.                                                                                                                                                                                                                                                                                                      |
| Db                    | 270 PAQDYLSLSQIT--VDKVSGDPMWIKY-SDTQVYGLNPEDIK--IGDIDKPNN 323         | SO                    | SEQUENCE FROM N.A.                                                                                                                                                                                                                                                                                                      |
| QY                    | 290 EITATGTYDNKNQKQITYTFDVKYENKAHLKLTSYIDSKVPPNNTKLDVEYKTAIS 349      | Query Match           | 18.1%; Score 559; DB 16; Length 1385;                                                                                                                                                                                                                                                                                   |
| Db                    | 324 ETIATKAKHTDANNLIVYTFEDVKYSGDPMWIDKNTV-----PSDLDSFTIPKID-NSG 381   | Best Local Similarity | 28.8%; Pred. No. 5. 9e-15;                                                                                                                                                                                                                                                                                              |
| QY                    | 350 SVNKTIVYEORPN--ENRTANLQSMFTNIDTKNT-----VQTIYINPLRSAKE 399         | Matches               | 177; Conservative 117; Mismatches 235; Indels 86; Gaps 27;                                                                                                                                                                                                                                                              |
| Db                    | 382 NTITKTTANIQYPDVYNEKNSIGAF--ETVSHVGNKENPGYYKOTIYINPSENSLTN         | QY                    | 8 SSDEEKNDV--INNNQSINTDDNNQIKEETNNYDGIEKRSEURTESTNTVDE-NEAT                                                                                                                                                                                                                                                             |
| Db                    | 400 TNVNI---SENDGEESTIIDSTIKVYKGDDNQMLPDSHRIVYDVS-EYEDVTDYVA 453      | Db                    | 114 STNKELNEATNTSASDNQSSDKVDMQOLNOEDNTKNDQNKEVNNSCGNETTSNGNKLIEKE                                                                                                                                                                                                                                                       |
| QY                    | 440 AKLKVKQAYHSSUPPNQGINKDQVTDIKYQPGRGYT--NKGYDVTNLKDVTN QYL 495      | QY                    | 64 FLQKIPQDNTLHLEEVEKESSESVESSNSSIDTAQQPSHTTINREVSQVTSDNVEDSHVSD                                                                                                                                                                                                                                                        |
| Db                    | 454 Q--LGNNNDYINFGNIDSPYIKVSKYDPNKKDVTQQTVMOTTINEYTGERTA              | Db                    | 115 SYVOSTGKVKEVSTAKSDEASPKNPSENEDNTQ--TISNQALQ-PDLLENKVNN                                                                                                                                                                                                                                                              |
| QY                    | 496 QKTYGDNNSAVTDFGNADSAVVMNTKFOYTNSSEPTLVQMAT-SSTGN-----KSV          | QY                    | 124 FANSKIKESNTESKGKENTIEQPN-KVEKESTTSQPSGYTNIDEKISNQDNLNPINEY                                                                                                                                                                                                                                                          |
| Db                    | 511 SYDNTAFTSTSGQGQGDLPPEKTYKIGDYWEVDVKDGIQNTNDNEKPLSVLVLITYP         | Db                    | 169 ---VQPTNEENKKD-----AKTEST-----LANKSDAIKSNETLIVNNNS 211                                                                                                                                                                                                                                                              |
| QY                    | 550 STGNALGFTNNMGGAG---QEVKIGNYWEVDTNKGQVEL--GKGVGNVTVV-FD            | QY                    | 183 ENKARPLSLTSQAOPSKRVTNOLAAEGS---NYNHLKVKDOSITEGDSBGGVKA                                                                                                                                                                                                                                                              |
| Db                    | 571 DGTSKSYR--TDEDGSKY 585                                            | Db                    | 212 ENNADILPKSTAKSNTMRMMA1OPNSIDSKNVNDLITSNTLVVDAKNNKIV 271                                                                                                                                                                                                                                                             |
| Db                    | 603 NNTNTKVGAEAVTKEDGSY 620                                           | QY                    | 239 HDAENLYDVFVEFDVKYSGDPMWIDKNT-----PSDLDSFTIPKID-NSG 291                                                                                                                                                                                                                                                              |
| RESULT                | 8                                                                     | Db                    | 272 QDYLŞLSQIT--VDDVKSGDPMWIKY-SDTQVYGLNPEDIK--IGDIDKPNN 325                                                                                                                                                                                                                                                            |
| Q99W47                | PRELIMINARY;                                                          | QY                    | 292 IATGTYDNKNQKQITYTFDVKYENKAHLKLTSYIDSKVPPNNTKLDVEYKTAIS 351                                                                                                                                                                                                                                                          |
| ID                    | 099W47                                                                | Db                    | 326 IATAKHTDANNLIVYTFEDVKYSGDPMWIDKNTV-----PSDLDSFTIPKID-NSG 383                                                                                                                                                                                                                                                        |
| AC                    | 099W47;                                                               | QY                    | 352 NRTTIVYEORPN--ENRTANLQSMFTNIDTKNT-----VQTIYINPLRSAKETN 401                                                                                                                                                                                                                                                          |
| DT                    | 01-JUN-2001 (TREMBREL. 17, Created)                                   | Db                    | 384 ITTADITYPAKEADNNSIGAF--ETVSHVGNVEDPOYINQVYVNPMDKLGK 441                                                                                                                                                                                                                                                             |
| DT                    | 01-JUN-2001 (TREMBREL. 17, Last sequence update)                      | QY                    | 402 VNISGNGDEGS-----TIDSPILKVKYGVQNQLDSNRIVYD--SEYDVTND--DYA 453                                                                                                                                                                                                                                                        |
| Db                    |                                                                       | Db                    | 442 LKVEAVHPKYPNQGINQNTNICKYRPGCYSYL--NKGYDVTNLKDVTDEPKNM 498                                                                                                                                                                                                                                                           |
| QY                    |                                                                       | QY                    | 454 QLGNNDYINFGNIDSPYIKVSKYDPNKKDVTQQTVMOTTINEYTGERTA 513                                                                                                                                                                                                                                                               |
| Db                    |                                                                       | Db                    | 499 TYGSNDSYLNDFRGDTISAVVMNTKFOYTNSSEPTLVQMATLSSGTN----KSVTG 552                                                                                                                                                                                                                                                        |
| QY                    |                                                                       | QY                    | 514 NTAFSTSSGQGQGDLPPEKTYKIGDYWEVDVKDGIQNTNDNEKPLSVLVLITYP 573                                                                                                                                                                                                                                                          |

|                                                  |                                                                                   |                                                            |      |    |     |                                                                |     |
|--------------------------------------------------|-----------------------------------------------------------------------------------|------------------------------------------------------------|------|----|-----|----------------------------------------------------------------|-----|
| Db                                               | 553                                                                               | NALGFTNNQSGGAG--QEVVKIGNYVWEDPNKNGVOEL-CEKGVGNYVTW-FDNNT   | 605  | Db | 592 | VKDUTSOFAPKVSADGTRVDINFARSMAANGKKYIVTQAVERPTGTGNVTT-EYWLTJRDGT | 649 |
| Qy                                               | 574                                                                               | SISVR--TDEDGKY                                             | 585  | Qy | 500 | INEYTGFRTASYDNTTAFSTSSGOGQGDLPPEKTYKIGDVWEDVKGJONTNDNEKP       | 559 |
| :                                                | :                                                                                 |                                                            |      | :  |     |                                                                |     |
| Db                                               | 606                                                                               | NTKVGEAVTKEDGSY                                            | 620  | Db | 650 | TN-TNDFYRGTKSTVTLNGSSTAQGDP--TYSLGDXWLDKNKNGIQ-DDDEKG          | 702 |
| RESULT                                           | 9                                                                                 |                                                            |      | Qy | 560 | LSNVLYLTVPGTSKS--VRTDEDGKYQFDGQ                                | 591 |
| QX                                               | OK114                                                                             | PRELIMINARY;                                               | PRT; | Qy |     |                                                                |     |
| ID                                               | OK114                                                                             |                                                            |      |    |     |                                                                |     |
| AC                                               | OK114:                                                                            |                                                            |      |    |     |                                                                |     |
| DR                                               | 01-OCT-2000 (TREMBLrel. 15, Created)                                              |                                                            |      |    |     |                                                                |     |
| DT                                               | 01-JUN-2001 (TREMBLrel. 17, Last sequence update)                                 |                                                            |      |    |     |                                                                |     |
| DE                                               | POTATIVE CELL-SURFACE ADHESIN SDRF.                                               |                                                            |      |    |     |                                                                |     |
| GN                                               | SDRF.                                                                             |                                                            |      |    |     |                                                                |     |
| OS                                               | Staphylococcus epidermidis                                                        |                                                            |      |    |     |                                                                |     |
| OC                                               | Bacteria; Firmicutes; Bacillus/Clostridium group;                                 |                                                            |      |    |     |                                                                |     |
| AN                                               | Bacillus/Staphylococcus group; Staphylococcus.                                    |                                                            |      |    |     |                                                                |     |
| RC                                               | NCBI_TaxID=1282;                                                                  |                                                            |      |    |     |                                                                |     |
| RP                                               | SEQUENCE FROM N.A.                                                                |                                                            |      |    |     |                                                                |     |
| RX                                               | MEDLINE-20310957; PubMed-1087818;                                                 |                                                            |      |    |     |                                                                |     |
| RA                                               | McCorm K.W., Hartford O., Davis S., Ni Eidhin D., Lina G.,                        |                                                            |      |    |     |                                                                |     |
| RT                                               | Speziale P., Foster T.J., Hook M.;                                                |                                                            |      |    |     |                                                                |     |
| RT                                               | "The serine-aspartate repeat (sar) protein family in Staphylococcus epidermidis"; |                                                            |      |    |     |                                                                |     |
| RL                                               | Microbiology 146:1535-1546(2000)..                                                |                                                            |      |    |     |                                                                |     |
| DR                                               | EMBL: AF245041; AAC7509.1;                                                        |                                                            |      |    |     |                                                                |     |
| DR                                               | InterPro: IPR001899; Gram_Pos_anchor                                              |                                                            |      |    |     |                                                                |     |
| PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1. |                                                                                   |                                                            |      |    |     |                                                                |     |
| SEQUENCE                                         | 1733 AA; 184720 MW; D8062EA169FD4E8 CRC64;                                        |                                                            |      |    |     |                                                                |     |
| Query Match                                      | 16.4%                                                                             | Score 506; DB 2; Length 1733;                              |      |    |     |                                                                |     |
| Best Local Similarity                            | 27.4%                                                                             | Score 506; DB 2; Length 1733;                              |      |    |     |                                                                |     |
| Matches                                          | 174;                                                                              | Conservative 101; Mismatches 276; Indels 84; Gaps 27;      |      |    |     |                                                                |     |
| Qy                                               | 7                                                                                 | PSDEE--KNVDVNNNOSINTDDNNOLIKKEETNNYDGIEKRSEDRTEST-----     | 54   |    |     |                                                                |     |
| Qy                                               | 135                                                                               | PTVNEEELAETKTKTSTWQDSETEKNSP-L-KDLNSSTTSKSKEDHSTPKQAMSTNK  | 193  |    |     |                                                                |     |
| Qy                                               | 55                                                                                | TVDENEA-TFLQKT-PODNTHLTEEVEKEESVSVSNS-----SIDTAQQPSHTT     | 103  |    |     |                                                                |     |
| Db                                               | 194                                                                               | SNLTDNSPQTQSEKTTSSQANNSTDNQAPSQQLDSRKPSEQVKVTKFNDEFTQDVHIT | 253  |    |     |                                                                |     |
| Db                                               | 104                                                                               | IN-REESVOTSNNEDSHVSDANSKIKESNTESKGENTTEQPNVKEDSTTSQSGY     | 162  |    |     |                                                                |     |
| Db                                               | 254                                                                               | TKLTPSVTSDSVNDK-QDYTRSAV---ASLGVSNETEATNAVRDNLKASRE        | 307  |    |     |                                                                |     |
| Qy                                               | 163                                                                               | NTIDEKI-----SNQDELNLNP--INEVNKARPLSTSQAOPSKRVTVNQLAE--     | 209  |    |     |                                                                |     |
| Db                                               | 308                                                                               | QIINERIAEALKRDFNSPDYQDGTPLALNRSKNSP-HKASP--RMMNSLAEPN      | 362  |    |     |                                                                |     |
| Qy                                               | 210                                                                               | QSNVNHILKVTQO-SITEGODSEGVKAHDENAENLYDVTFEVDDKVSCDMVQID     | 267  |    |     |                                                                |     |
| Db                                               | 363                                                                               | SGKVNNDVKVKTINPTSLNKSNNHANVWIWSNEQENPLKANYELODSIKGGDFTIKY  | 422  |    |     |                                                                |     |
| Qy                                               | 268                                                                               | KNTVPSDITSDSTIPKIKDNSSEIATGTYDNNKQIYTFTDVIDYKENTRAHLKLTSY  | 327  |    |     |                                                                |     |
| Db                                               | 423                                                                               | QYRPGGLELPALKTQIQRSKDGSIVANGVYDQTNTTTFNIVDQYQNTGSDLIAT     | 482  |    |     |                                                                |     |
| Qy                                               | 328                                                                               | IHKSKVUNNTKLDVEKTAALSVNKVITVEQRPNENRNTALQSMPTNTDKHNTVEQT   | 387  |    |     |                                                                |     |
| Db                                               | 483                                                                               | PRTETAKDNQNPMEVITANEVVKKTFIDGKNTKTT--AAVANVDVNNHNEV        | 539  |    |     |                                                                |     |
| Qy                                               | 388                                                                               | IYINPLRYSAKETVNNTSGNGDBGSTIDDSI--IKVYKGDNQNLPS-NRIVDYE     | 443  |    |     |                                                                |     |
| Db                                               | 540                                                                               | VYLNNONNPKAKY-----FSTVKNGEFTPEGEKVYETDNTMWDSEFPNDLSSN      | 591  |    |     |                                                                |     |
| Qy                                               | 444                                                                               | YEDVNTDDYAQI-GNNMDVNTIFGNT--DSPIYKIVSKVPKNDYDTTQVNMOTT     | 499  |    |     |                                                                |     |

|          |                                                                                                               |                                                             |              |
|----------|---------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|--------------|
| Db       | 298                                                                                                           | NLI-TFTDQVTVNKNNTGQISITPGYIDBPKNVHTG--KVNLETSIGQATKKIVIVDEA | 353          |
| Oy       | 362                                                                                                           | PNNRNTANLQSMFTNIDTKNHTVQFQIINPLRYSAKETNNN--ISGN--GDEGSTID   | 416          |
|          |                                                                                                               | : ; :       :     :     :     :     :     :     :           |              |
|          | 356                                                                                                           | YGEFRNLISKIGTIPQDIDKRNNTYQTVWVNNP---SSDQWVDYLRSIGSPGSNSVTD  | 411          |
| Db       | 417                                                                                                           | D-STTIKVYKVGDQNOLPPSNRIVDYESEVDVNDYAQLGNNNDVNINF---NIDSP    | 471          |
|          | : :                                                                                                           | :     : :     :     :     :     :     :     :               |              |
| Oy       | 412                                                                                                           | EONTSIKVYKVKEKAHDTYYV--DPSNEYDVDSVKITPEKGIQINFNTSDDQINSP    | 470          |
| Db       | 472                                                                                                           | YIKLISKVNPDKDVTQTOQVIMOTTNENYGEFRIS--DNTIIRSTSSGQGQDL       | 529          |
|          | :: :                                                                                                          | :     : : :: :     :     :     :     :     :                |              |
| Oy       | 530                                                                                                           | PPEKTYKIGD----YVWEVDYKD 548                                 |              |
| Db       | 471                                                                                                           | YVWVINGHVDPNSN-----NLYLRSTLVGYDSDNSNFRVSMANDNEVEYHAGSGNGDGD | 524          |
|          | 525                                                                                                           | KPVIPDQPGSDSDAYSDSDADSD 548                                 |              |
|          |                                                                                                               |                                                             |              |
| RESULT   | 12                                                                                                            |                                                             |              |
| ID       | 086487                                                                                                        | PRELIMINARY;                                                | PRT; 947 AA. |
| AC       | 086487;                                                                                                       |                                                             |              |
| DT       | 01-NOV-1998 (TREMBLrel. 08, Created)                                                                          |                                                             |              |
| DT       | 01-NOV-1998 (TREMBLrel. 08, Last sequence update)                                                             |                                                             |              |
| DT       | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                                                           |                                                             |              |
| DE       | SDRC PROTEIN.                                                                                                 |                                                             |              |
| GN       | SDRC.                                                                                                         |                                                             |              |
| OS       | Staphylococcus aureus.                                                                                        |                                                             |              |
| OC       | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                             |                                                             |              |
| OC       | Bacillus/Staphylococcus group; Staphylococcus.                                                                |                                                             |              |
| OX       | NCBI_TAXID:1280;                                                                                              |                                                             |              |
| RN       | [1]                                                                                                           |                                                             |              |
| RP       | SEQUENCE FROM N.A.                                                                                            |                                                             |              |
| RC       | STRAIN=NEWMAN;                                                                                                |                                                             |              |
| RX       | MEDLINE-9908700; Pubmed=9984231;                                                                              |                                                             |              |
| RA       | Josefsson E., McCrea K., Ni Elinin D., O'Connell D., Cox J., Hook M.,                                         |                                                             |              |
| RA       | Foster T.J.;                                                                                                  |                                                             |              |
| RT       | "Three new members of the serine-aspartate repeat protein multigene family of <i>Staphylococcus aureus</i> "; |                                                             |              |
| RT       | Microbiology 144:387-395(1998).                                                                               |                                                             |              |
| RL       | EMBL: Ad05645; CAA06501; -.                                                                                   |                                                             |              |
| DR       | INTERPRO: IPR01899; Gram_pos_anchor.                                                                          |                                                             |              |
| DR       | Pfam: PF00746; Gram_pos_anchor; 1.                                                                            |                                                             |              |
| PROTEIN: | PS00043; GRAM_POS_ANCHOR; UNKNOWN <sup>1</sup> .                                                              |                                                             |              |
| SEQUENCE | 947 AA; 102888 MW; 3C6ELDE3121554 CRC64;                                                                      |                                                             |              |

|                                                                     |                                                                                                                                    |                                                             |         |
|---------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------|---------|
| Db                                                                  | 300                                                                                                                                | QVAFAKRNNTDKTAYKNEVTLGNDTVSEELIVDY--GNKKAQOPLSISSTNVINNEDLS | 356     |
| Db                                                                  | 308                                                                                                                                | VIDS-DGNYIYTFFDVNTRKDVKATLMPAYD---PENVKKGIVYLATGIGSTAN      | 362     |
| Qy                                                                  | 384                                                                                                                                | VEOTIYIN-PLRYSAKETNV-NTSNGNGDEGSTIDDSITIKVKGDNQNL----PDSN   | 436     |
| Db                                                                  | 357                                                                                                                                | RNMTAYWVQPKNVTKOTFVNLT----GYKENPNAKNFKIVETDQNQFDSTFDTS      | 411     |
| Qy                                                                  | 437                                                                                                                                | RVDYSEVEDVNDYAGLGNNDVNIFGNIDS--PTIKVI----SKVPPNKKDTT        | 489     |
| Db                                                                  | 412                                                                                                                                | KLKDVTOFDVVI--YSNDNKTAVDLMKGQFSNSNKQYIQQVAPDNSTDNGKIDY--    | 466     |
| Qy                                                                  | 490                                                                                                                                | IQQVVTMOTTINVTGEFRASVNTIAFSTSSQGQGDLPPEKTYKIGDYWDVDKDG      | 549     |
| Qy                                                                  | 467                                                                                                                                | -----TLDTKTWSW--SNSTSVNGSSTANGD-----QKQYNLGDIYWDTNKDG       | 511     |
| Qy                                                                  | 550                                                                                                                                | TQTNNDNERPLSLNVLYTYPDTS-KSVRTEDEGKTFQDFGV                   | 590     |
| Qy                                                                  | 512                                                                                                                                | KODA--NEKGIGKVYVILKDSNGKELDRITDENGKTOFTGL                   | 551     |
| ..RESULT 13                                                         |                                                                                                                                    |                                                             |         |
| Q33653                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 933 AA. |
| ID                                                                  | Q33653;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33653_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-NOV-1996 (Tremblrel. 01, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-NOV-1996 (Tremblrel. 01, Last sequence update)                                                                                  |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last annotation update)                                                                                |                                                             |         |
| DE                                                                  | CLUMPING FACTOR.                                                                                                                   |                                                             |         |
| OS                                                                  | Staphylococcus aureus.                                                                                                             |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=1280;                                                                                                                   |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE-9422142; PubMed=8170386;                                                                                                   |                                                             |         |
| RA                                                                  | McDevitt D., Francois P., Vaudaux P., Foster T.J.,                                                                                 |                                                             |         |
| RA                                                                  | "Molecular characterization of the clumping factor(fibrogen receptor of Staphylococcus aureus.", Mol. Microbiol. 11:237-248(1994). |                                                             |         |
| RA                                                                  | EMBL: Z18852; CA0V93041; -.                                                                                                        |                                                             |         |
| DR                                                                  | InterPro: IPR00155; BPD_transp.                                                                                                    |                                                             |         |
| DR                                                                  | InterPro: IPR001890; Gram_pos_anchor.                                                                                              |                                                             |         |
| DR                                                                  | PROSITE: PS00402; BPD_TRANSP_INN MEMBR: UNKNOWN_1;                                                                                 |                                                             |         |
| DR                                                                  | PROSITE: PS00343; GRAM_PCS_ANCHORING; UNKNOWN_1;                                                                                   |                                                             |         |
| DR                                                                  | SEQUENCE: 933 AA; 97058 MW; EB51A6DE2FF/59F4 CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 2; Length 933;                     |                                                                                                                                    |                                                             |         |
| Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  |                                                                                                                                    |                                                             |         |
| Best Local Similarity 26.6%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 14                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             |         |
| OS                                                                  | Staphylococcus aureus (strain Mu50).                                                                                               |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=158678;                                                                                                                 |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 16; Length 935;                    |                                                                                                                                    |                                                             |         |
| Matches 152; Conservative 109; Mismatches 224; Indels 102; Gaps 27; |                                                                                                                                    |                                                             |         |
| Best Local Similarity 25.9%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 15                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             |         |
| OS                                                                  | Staphylococcus aureus (strain Mu50).                                                                                               |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=158678;                                                                                                                 |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 16; Length 935;                    |                                                                                                                                    |                                                             |         |
| Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  |                                                                                                                                    |                                                             |         |
| Best Local Similarity 26.6%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 16                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             |         |
| OS                                                                  | Staphylococcus aureus (strain Mu50).                                                                                               |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=158678;                                                                                                                 |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 16; Length 935;                    |                                                                                                                                    |                                                             |         |
| Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  |                                                                                                                                    |                                                             |         |
| Best Local Similarity 26.6%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 17                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             |         |
| OS                                                                  | Staphylococcus aureus (strain Mu50).                                                                                               |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=158678;                                                                                                                 |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 16; Length 935;                    |                                                                                                                                    |                                                             |         |
| Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  |                                                                                                                                    |                                                             |         |
| Best Local Similarity 26.6%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 18                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             |         |
| OS                                                                  | Staphylococcus aureus (strain Mu50).                                                                                               |                                                             |         |
| OC                                                                  | Bacteria; Firmicutes; Bacillus/Clostridium group;                                                                                  |                                                             |         |
| OC                                                                  | Bacillus/Staphylococcus group; Staphylococcus.                                                                                     |                                                             |         |
| OC                                                                  | NCBI_TaxID=158678;                                                                                                                 |                                                             |         |
| RN                                                                  | [1]                                                                                                                                |                                                             |         |
| RC                                                                  | SEQUENCE FROM N.A.                                                                                                                 |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| Query Match 14.6%; Score 452; DB 16; Length 935;                    |                                                                                                                                    |                                                             |         |
| Matches 154; Conservative 105; Mismatches 234; Indels 86; Gaps 26;  |                                                                                                                                    |                                                             |         |
| Best Local Similarity 26.6%; Pred. No. 7.3e-11;                     |                                                                                                                                    |                                                             |         |
| SEQUENCE FROM N.A.                                                  |                                                                                                                                    |                                                             |         |
| RP                                                                  | [1]                                                                                                                                |                                                             |         |
| RX                                                                  | MEDLINE=21311952; PubMed=11418146;                                                                                                 |                                                             |         |
| RA                                                                  | Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,                                                                 |                                                             |         |
| RA                                                                  | Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,                                                                       |                                                             |         |
| RA                                                                  | Kanamori M., Matsumura H., Maruyama A., Murakami H., Hosoyama A.,                                                                  |                                                             |         |
| RA                                                                  | Mizutani-Uji Y., Takahashi N.K., Savano T., Inoue R.-I., Kaito C.,                                                                 |                                                             |         |
| RA                                                                  | Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,                                                                          |                                                             |         |
| RA                                                                  | Kanehisa M., Yamashita A., Oshima K., Funaya K., Yoshino C., Shiba T.,                                                             |                                                             |         |
| RA                                                                  | Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,                                                                                |                                                             |         |
| RT                                                                  | "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.", Lancet 357:1225-1240(2001);                             |                                                             |         |
| RL                                                                  | EMBL: AP003360; BAB56973.1; -.                                                                                                     |                                                             |         |
| DR                                                                  | Complete proteome.                                                                                                                 |                                                             |         |
| KW                                                                  | SEQUENCE: 935 AA; 96950 MW; DC5A2D92C83BA91C CRC64;                                                                                |                                                             |         |
| ..RESULT 19                                                         |                                                                                                                                    |                                                             |         |
| Q33205                                                              | PRELIMINARY;                                                                                                                       | PRT;                                                        | 935 AA. |
| ID                                                                  | Q33205;                                                                                                                            |                                                             |         |
| AC                                                                  | Q33205_C;                                                                                                                          |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Created)                                                                                               |                                                             |         |
| DT                                                                  | 01-DEC-2001 (Tremblrel. 19, Last sequence update)                                                                                  |                                                             |         |
| DE                                                                  | FIBRINOGEN-BINDING PROTEIN.                                                                                                        |                                                             |         |
| GN                                                                  | FNB OR SAV0811.                                                                                                                    |                                                             | </td    |

Db 245 SGTIVVPHQAGVVKLNKGFSVPNSAVKGDTEKITVPKBLNLNGVTSTAKVPPIMAGD-QV 303  
 QY 292 IATGTYDNKNKQIYTTFDYDVKYENIKAHKLITSYIDSKVPPNNKL-DVEYKTL-- 348  
 Db 304 LANGVIDS-DGNYIYTIDVDRKENTANITNPAYID---PENVTKIGNVLTGIGT 358  
 QY 349 SSVNKTIVYEOPRNENRANTNQSMFTNDTAKHTVQDTCVYINPLRSAKENV---- 402  
 Db 359 NTASKTVLIDYERQGOFHNLSTIKGTIDQIDKNTNQTYTIQVYNE----SGDNVLPLALT 413  
 QY 403 -NISGNGDEGSYIIDDSTIJKVKGDNQLDPSNRIDYSFEDVNDYDVAQGNNDV 461  
 Db 414 GNLPNPKNSNALIDAKNIDIKYRV-DNANDISESYVNVPSDFEVNQVRISFPNQY 472  
 QY 462 NINF---GNIDSPYIJKVSKYDPNKDDTTIQTQVYMQTHINEYGEF--RTASYDT 515  
 Db 473 KVEPTDDQDQITPYIIVVNGHIDPASTG----DIALSRTFYGDSNFWRMSNDNE 526  
 QY 516 IAFSTSSQGQG-DLP--PEKTYKIGD--VWEDVNDK-GIONTNDN 556  
 Db 527 VAFNNGSGSGDGLDKPVVPEQDPEGEIEPIEDSDSDPGSGSDS 573

RESULT 15  
 Q9VJ4 PRELIMINARY; PRT; 989 AA.  
 ID Q9VJ4  
 AC :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|  
 DT 01-JUN-2001 (TREMBREL, 17, Last sequence update)  
 DE FIBRINOGEN-BINDING PROTEIN A, CLUMPING FACTOR.  
 GN CLEA OR SA0742.  
 OS Staphylococcus aureus (strain N315).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OX NEBI\_TAXID=158879;  
 RN {1}  
 RP SQQUENCE FROM N.A.  
 RX MEDLINE=21311952; PubMed=11418146;  
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
 RA Cui L., Oguchi A., Aoki K.I., Negai Y., Liang J., Ito T., Kanamori M.,  
 RA Matsunaru H., Matuyama A., Murakami H., Hosoyama A., Miutani-Uji Y.,  
 RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Satomizu K.,  
 RA Hirakawa H., Kuhara S., Goto S., Rabizadeh J., Kanenisa M.,  
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,  
 RA Ogasawara N., Hayashi H., Hiramatsu K.;  
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*  
 aureus"; Lancet 357:1225-1240(2001).  
 RL EMBL; AP003131; BAB41975.1;  
 InterPro; IPR000515; BPD\_transp.  
 InterPro; IPR000189; Gram\_pos\_anchor.  
 PROSITE; PS00402; BPD\_TRANS\_INN\_MEMR; UNKNOWN\_1.  
 Complete proteome; PS00343; GRAM\_POS\_ANCHORING;  
 UNKNOWN\_1.  
 SEQUENCE 989 AA; 102407 MW; DA6E807539623467 CRC64;

Query Match 14.6%; Score 452; DB 16; Length 989;  
 Best Local Similarity 25.9%; Pred. No. 7.7e-11; Gaps 27;  
 Matches 152; Conservative 109; Mismatches 224; Indels 102; Gaps 27;

QY 8 SDDEEKDVINNNQSIINDDNNQIKEETNNYDGIERSEDRTESTINVDENEATFLQK 67  
 Db 51 SDEEKDVINNNQSIINDDNNQIKEETNNYDGIERSEDRTESTINVDENEATFLQK 67  
 QY 68 TDQDNTHLTEEKEKESSEVSESSNSIDTAQQPSHTINREESVOTSONVDSHVSDFANS 127  
 Db 92 NP----AQETQSSNTATEETPTVGETTINQANTFATTUS-SNTNAELVN- 143  
 QY 128 KIKESENTEGKENTIOPNPKMEDSTSOPSYTNIDEKIISNODELNPINEYKA 186  
 Db 144 --QTSNETTSNDTNTV-----SSVNSPONSTNAENVSTQDSTEATPSN--NES 189

QY 187 RPLSTTS-----OPSIKRVTVNOLAA-----EGGSNVNHLIKTVTOSITEGYDD 231  
 Db 190 APONTDASNKDVVSQANFSTPRMRASLAAVADAPAGTDTN- QLTDKVTT--ID 244  
 QY 232 SECVIKADAENLYDVFEDDKVKGSDTMVTDKNTVPSLDTSFTIPKIDNSGET 291  
 Db 245 SGTIVVPHQAGVVKLNKGFSVPNSAVKGDTEKITVPKBLNLNGVTSTAKVPPIMAGD-QV 303  
 QY 292 IATGTYDNKNKQIYTTFDYDVKYENIKAHKLITSYIDSKVPPNNKL-DVEYKTL- 348  
 Db 304 LANGVIDS-DGNYIYTIDVDRKENTANITNPAYID---PENVTKIGNVLTGIGT 358  
 QY 349 SSVNKTIVYEOPRNENRANTNQSMFTNDTAKHTVQDTCVYINPLRSAKENV---- 402  
 Db 359 NTASKTVLIDYERQGOFHNLSTIKGTIDQIDKNTNQTYTIQVYNE----SGDNVLPLALT 413  
 QY 403 -NISGNGDEGSYIIDDSTIJKVKGDNQLDPSNRIDYSFEDVNDYDVAQGNNDV 461  
 Db 414 GNLPNPKNSNALIDAKNIDIKYRV-DNANDISESYVNVPSDFEVNQVRISFPNQY 472  
 QY 462 NINF---GNIDSPYIJKVSKYDPNKDDTTIQTQVYMQTHINEYGEF--RTASYDT 515  
 Db 473 KVEPTDDQDQITPYIIVVNGHIDPASTG----DIALSRTFYGDSNFWRMSNDNE 526  
 QY 516 IAFSTSSQGQG-DLP--PEKTYKIGD--VWEDVNDK-GIONTNDN 556  
 Db 527 VAFNNGSGSGDGLDKPVVPEQDPEGEIEPIEDSDSDPGSGSDS 573

Search completed: July 30, 2002, 10:40:30  
 Job time: 569 sec

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